REMARKS

Applicant's attorney Bentley Olive conducted a Telephone Interview with Examiner Mizrahi on February 15, 2006 regarding the fax submission of Exhibits A and B on December 15, 2005. Applicant's attorneys sincerely appreciate Examiner Mizrahi's time and consideration in participating in the Telephone Interview.

Examiner Mizrahi was unable to read the Exhibits and suggested mailing the Exhibits. Attached are Exhibit A and B. Please note the Exhibits can be pieced together by referring to the attached grids.

By submission of the attached copies of Exhibits A and B, applicant respectfully submits that Amendment B is fully responsive to the Official Action dated March 1, 2005. Further, applicant respectfully requests reconsideration of Amendment B.

CONCLUSION

In light of the above amendments and remarks, it is respectfully submitted that the present application is now in proper condition for allowance, and such action is earnestly solicited.

If any small matter should remain outstanding after the Patent Examiner has had an opportunity to review the above Remarks, the Patent Examiner is respectfully requested to telephone the undersigned patent attorney in order to resolve these matters and avoid the issuance of another Official Action.

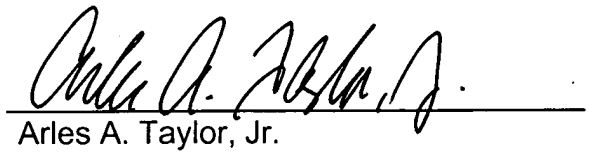
BEST AVAILABLE COPY

DEPOSIT ACCOUNT

The Commissioner is hereby authorized to charge any fees associated with the filing of this correspondence to Deposit Account No. **50-0426**.

Respectfully submitted,

JENKINS, WILSON, TAYLOR & HUNT, P.A.

Date: 02/22/2006 By: 

Arles A. Taylor, Jr.
Registration No. 39,395
Customer No. 25297

AAT/BJO/alb

1392/10/22

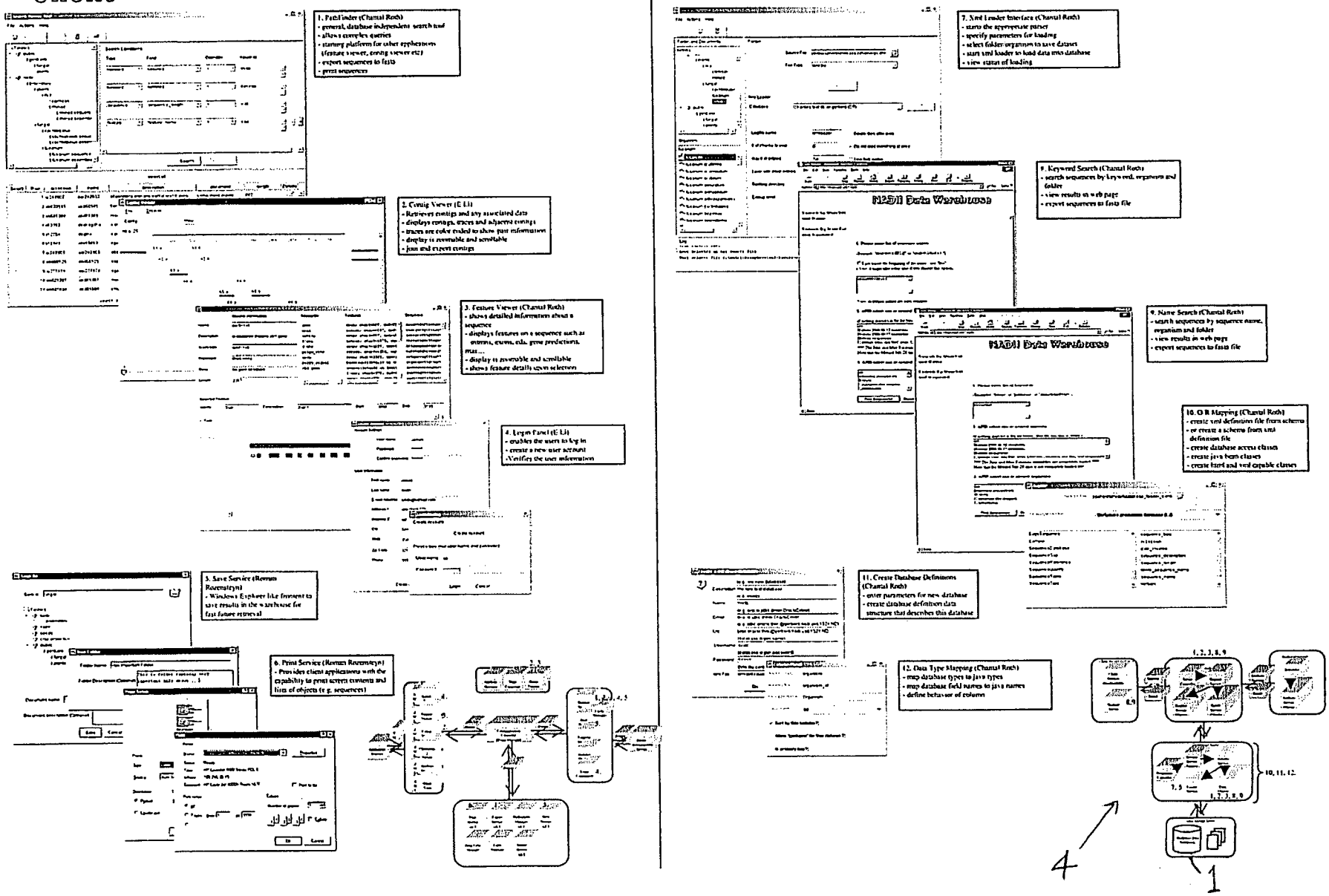
Exhibit A

BioSphere User and Administration Tools

Chantal Roth, E Li, Roman Rozenstein

Client

Server



BioSphere User and Administration Tools

Chantal Roth, E Li, Roman Rozensteyn

Client

Server

A1

B1

C1

D1

1. PathFinder (Chantal Roth)
- general, database independent search tool
- allows complex queries
- starting platform for other applications (feature viewer, contig viewer etc)
- export sequences to fasta
- print sequences

7. Xml Loader Interface (Chantal Roth)
- starts the appropriate parser
- specify parameters for loading
- select folder/organism to save dataset
- start xml loader to load data into database
- view status of loading

A2

B2

C2

D2

2. Contig Viewer (E Li)
- Retrieves contigs and any associated data
- displays contigs, traces and adjacent contigs
- traces are color coded to show pair information
- display is zoomable and scrollable
- Join and export contigs

8. Keyword Search (Chantal Roth)
- search sequences by keyword, organism and folder
- view results in web page
- export sequences to fasta file

3. Feature Viewer (Chantal Roth)
- shows detailed information about a sequence
- displays features on a sequence such as introns, exons, cds, gene predictions, rnas...
- display is zoomable and scrollable
- shows feature details upon selection

9. Name Search (Chantal Roth)
- search sequences by sequence name, organism and folder
- view results in web page
- export sequences to fasta file

4. Login Panel (E Li)
- enables the users to log in
- create a new user account
- Verifies the user information

10. O/R Mapping (Chantal Roth)
- create xml definition file from schema
- or create a schema from xml definition file
- create database access classes
- create java bean classes
- create html and xml capable classes

A3

B3

C3

D3

5. Save Service (Roman Rozensteyn)
- Windows Explorer like frontent to save results in the warehouse for fast future retrieval

11. Create Database Definitions (Chantal Roth)
- enter parameters for new database
- create database definition data structure that describes this database

6. Print Service (Roman Rozensteyn)
- Provides client applications with the capability to print screen contents and lists of objects (e.g. sequences)

12. Data Type Mapping (Chantal Roth)
- map database types to java types
- map database field names to java names
- define behavior of column

A4

B4

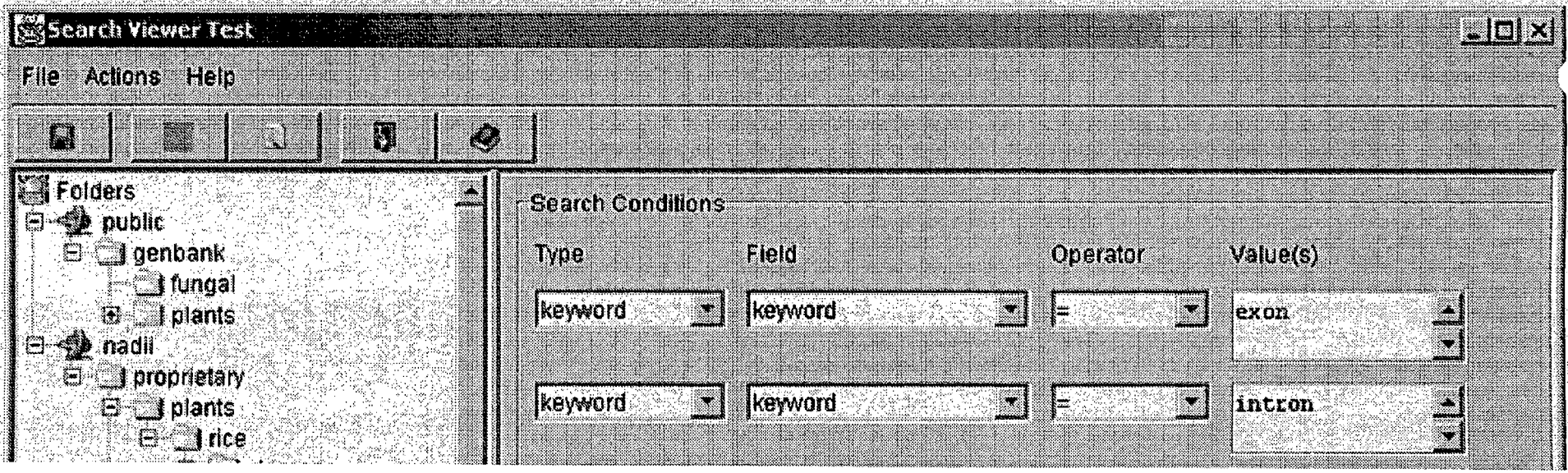
C4

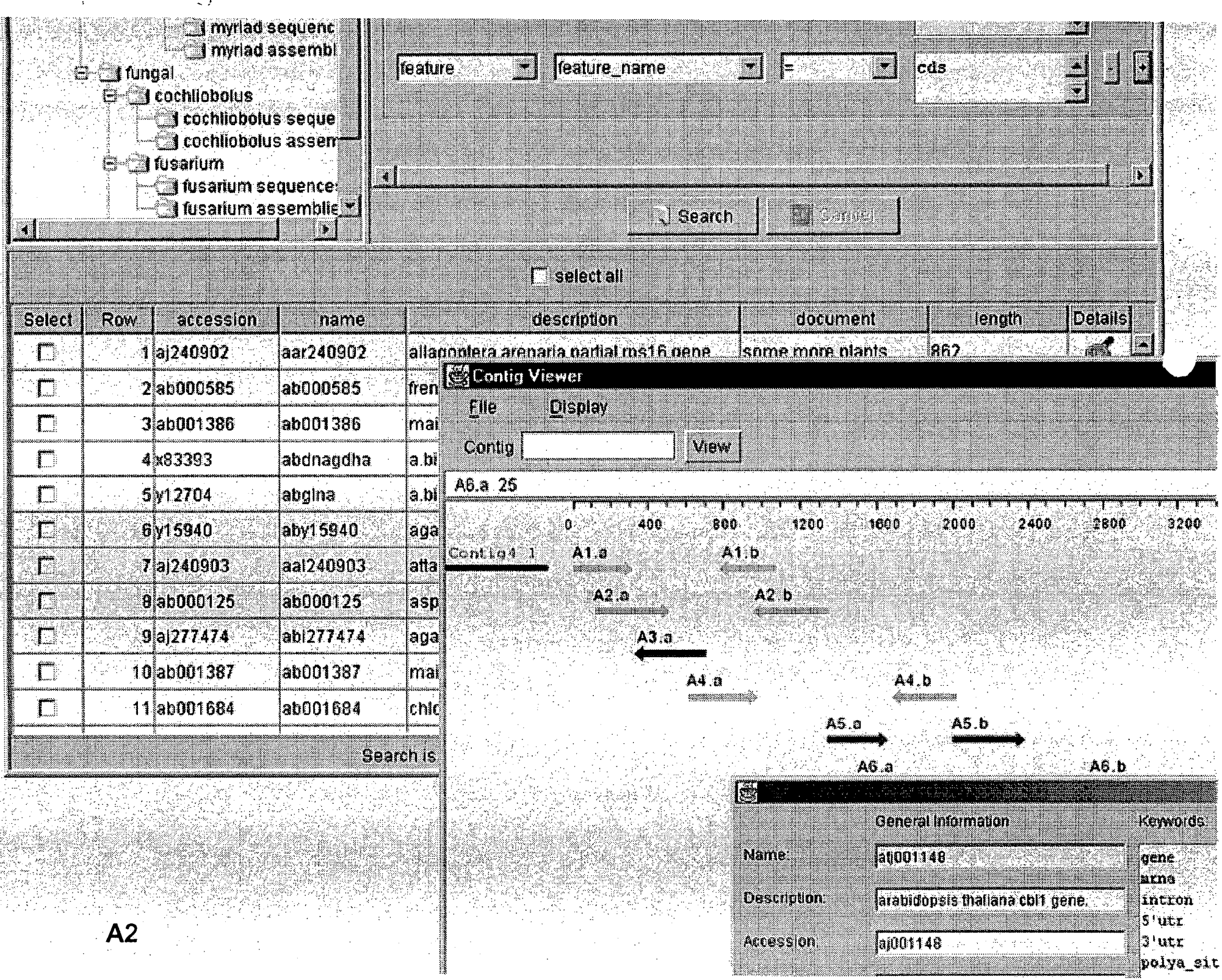
D4

BioSpl

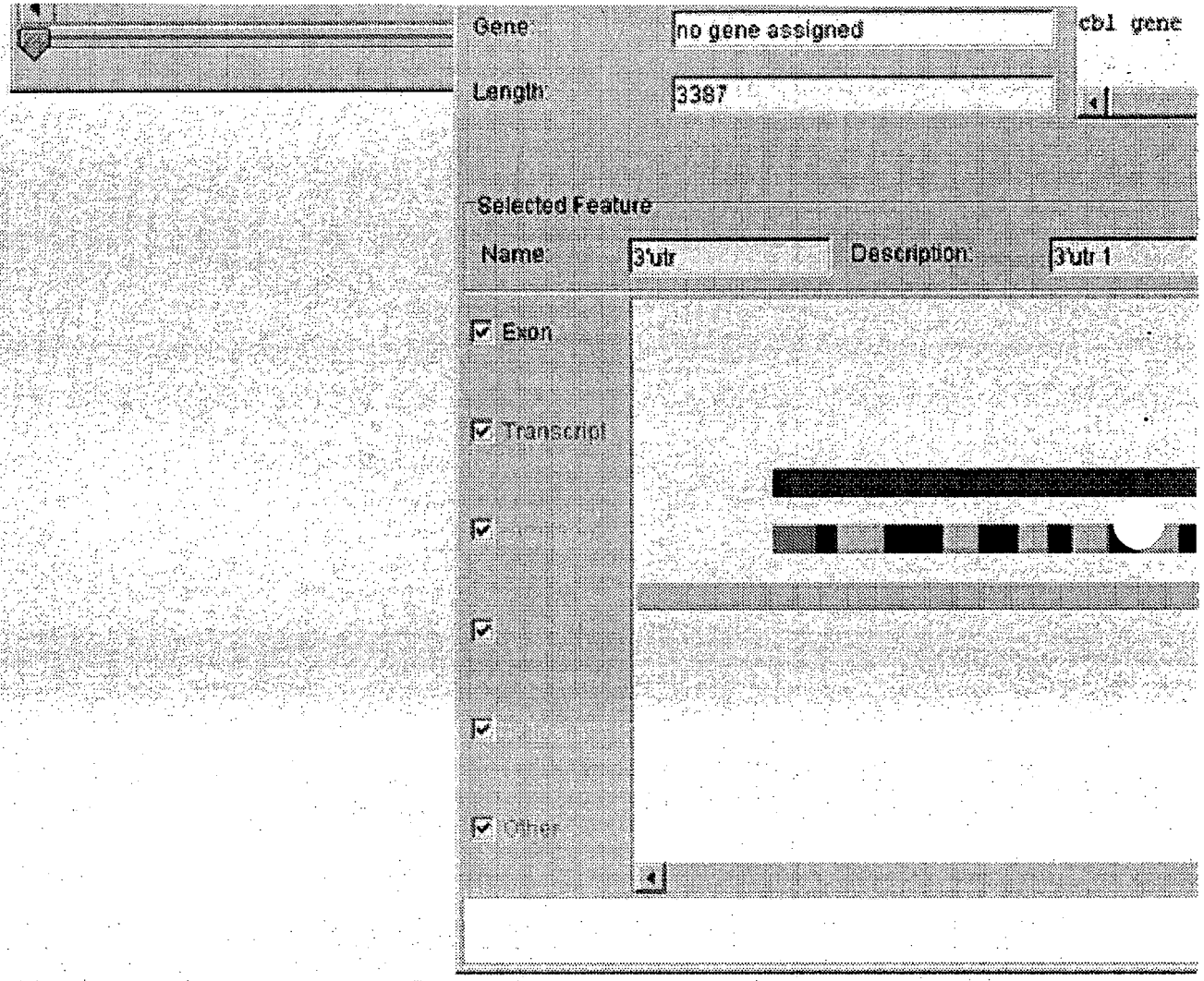
Client

A1

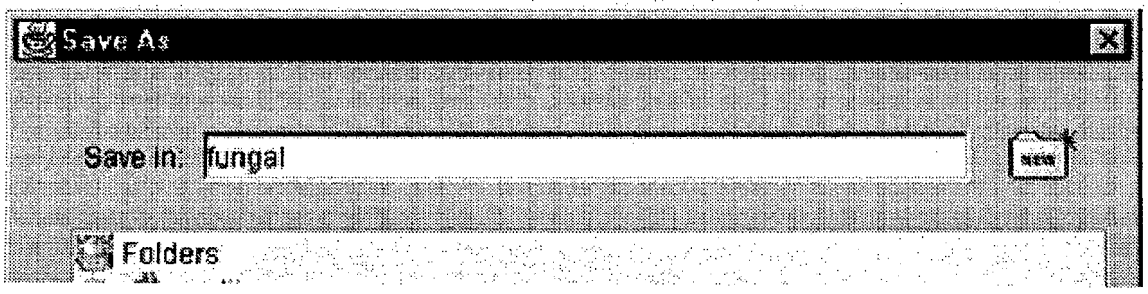



myriad sequenc
myriad assembl
fungal
cochliobolus
cochliobolus seque
cochliobolus assen
fusarium
fusarium sequence
fusarium assemblie
feature
feature_name
=
cds
Search
Cancel
select all
Select
Row
accession
name
description
document
length
Details
1 aj240902 aar240902 allagoptera arenaria partial rps16 gene some more plants 862
2 ab000585 ab000585 fren
3 ab001386 ab001386 mai
4 x83393 abdnagdha a.bi
5 y12704 abglna a.bi
6 y15940 aby15940 aga
7 aj240903 aal240903 atta
8 ab000125 ab000125 asp
9 aj277474 abl277474 aga
10 ab001387 ab001387 mai
11 ab001684 ab001684 chlc
Search is
Contig Viewer
File
Display
Contig
View
A6.a 25
0
400
800
1200
1600
2000
2400
2800
3200
Contig4 1
A1.a
A1.b
A2.a
A2.b
A3.a
A4.a
A4.b
A5.a
A5.b
A6.a
A6.b
General Information
Keywords:
Name:
at001148
Description:
arabidopsis thaliana cbl1 gene.
Accession:
aj001148
gene
mrna
intron
5'utr
3'utr
polya_sit

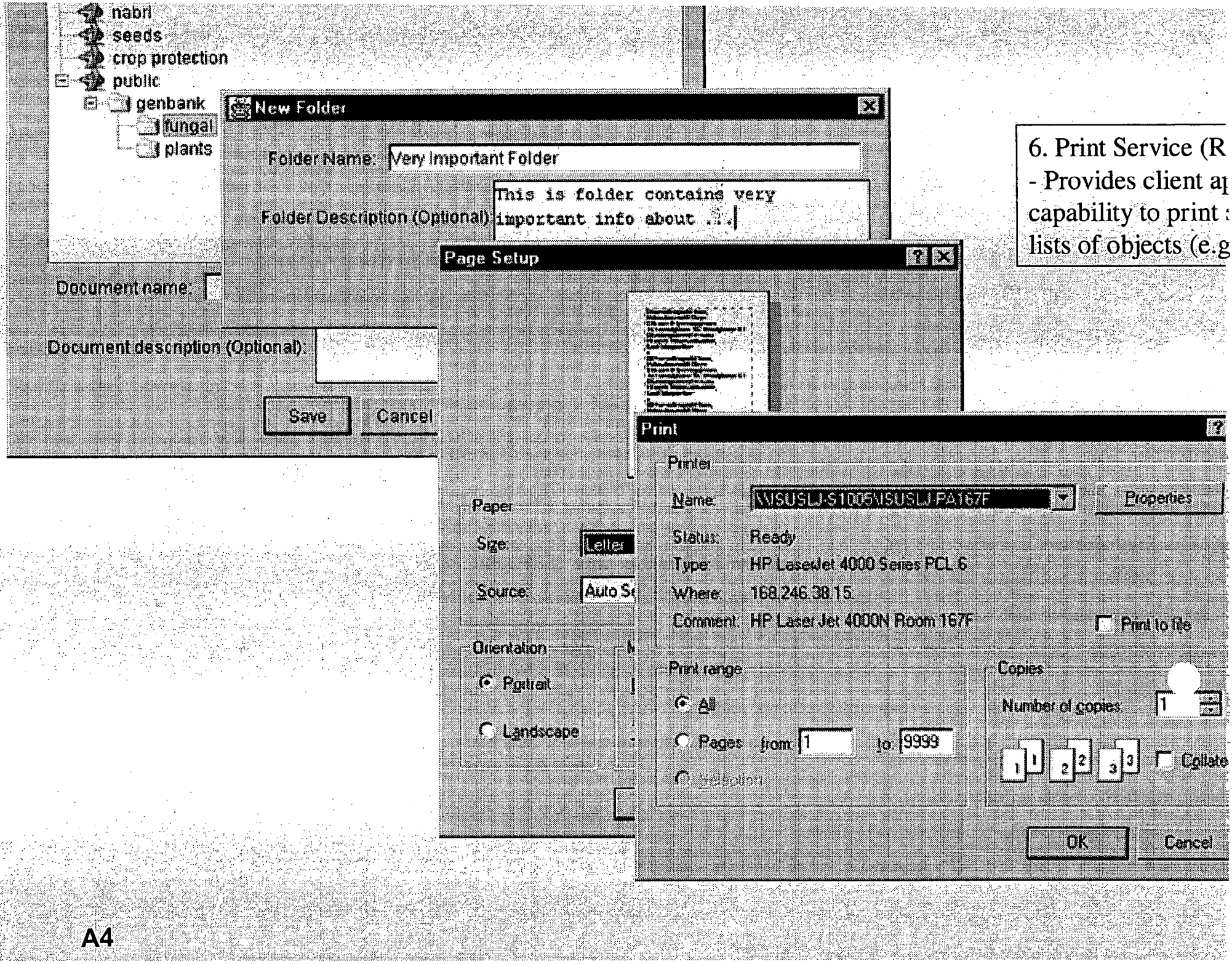
A2



A3



5. Save Service (Roman Rozensteyn) - Windows Explorer like frontent to save results in the warehouse for fast future retrieval



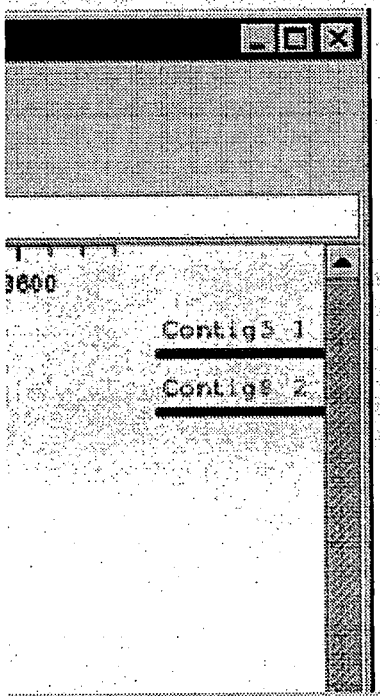
6. Print Service (R
- Provides client ap
capability to print
lists of objects (e.g

A4

ere User and A

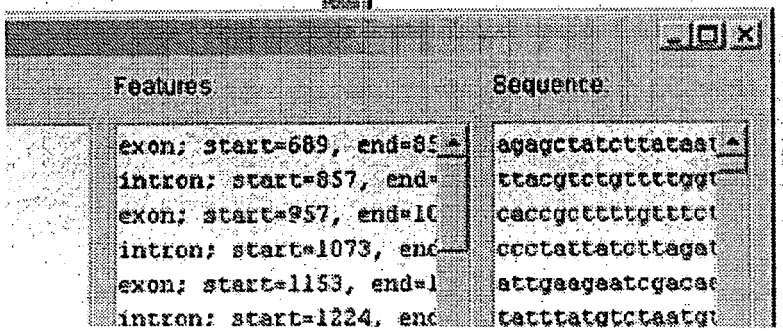
Chantal Roth, E Li, R

PathFinder (Chantal Roth)
eneral, database independent search tool
llows complex queries
arting platform for other applications
eature viewer, contig viewer etc)
xport sequences to fasta
rint sequences

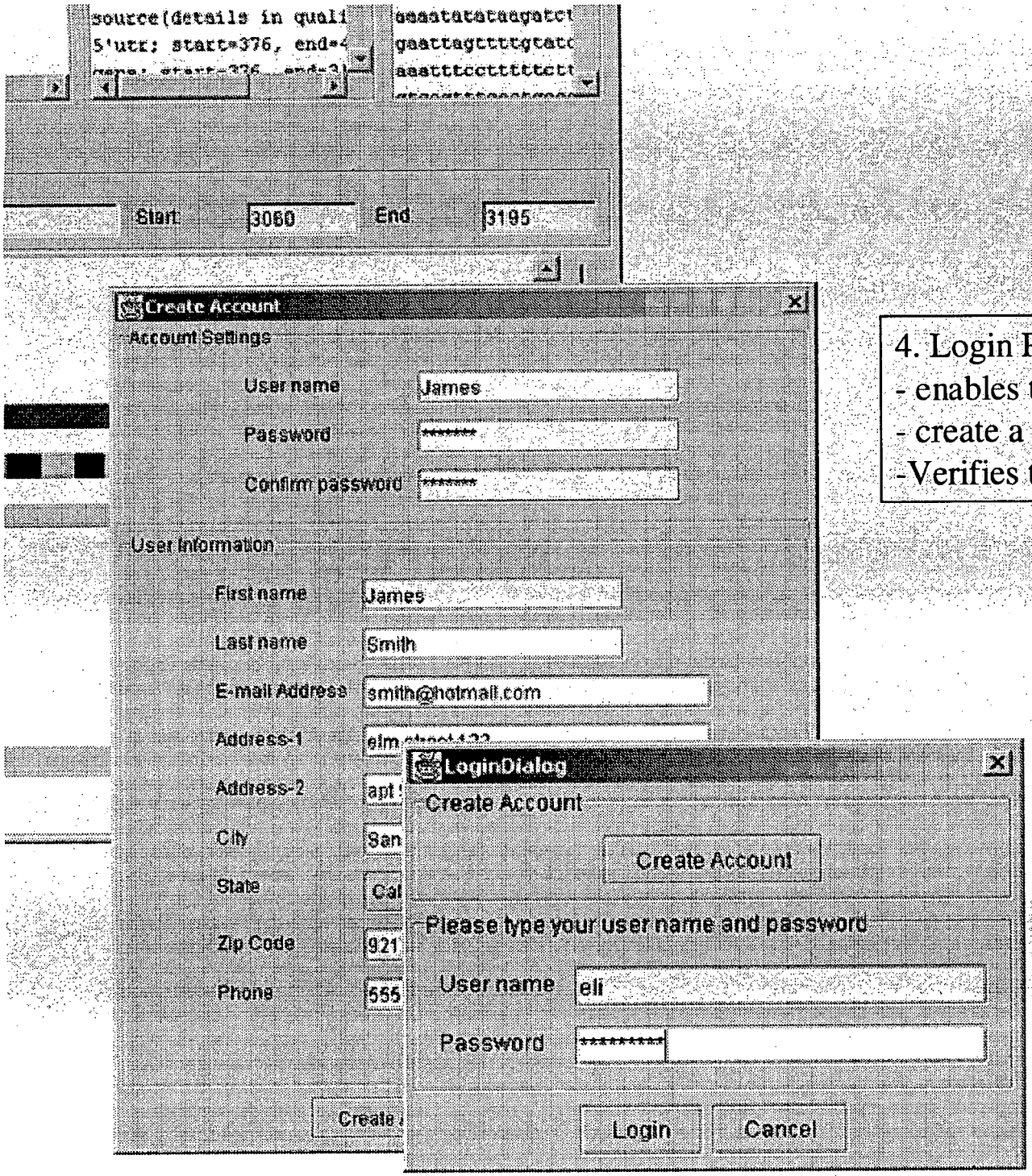


2. Contig Viewer (E Li)
- Retrieves contigs and any associated data
- displays contigs, traces and adjacent contigs
- traces are color coded to show pair information
- display is zoomable and scrollable
- join and export contigs

B2

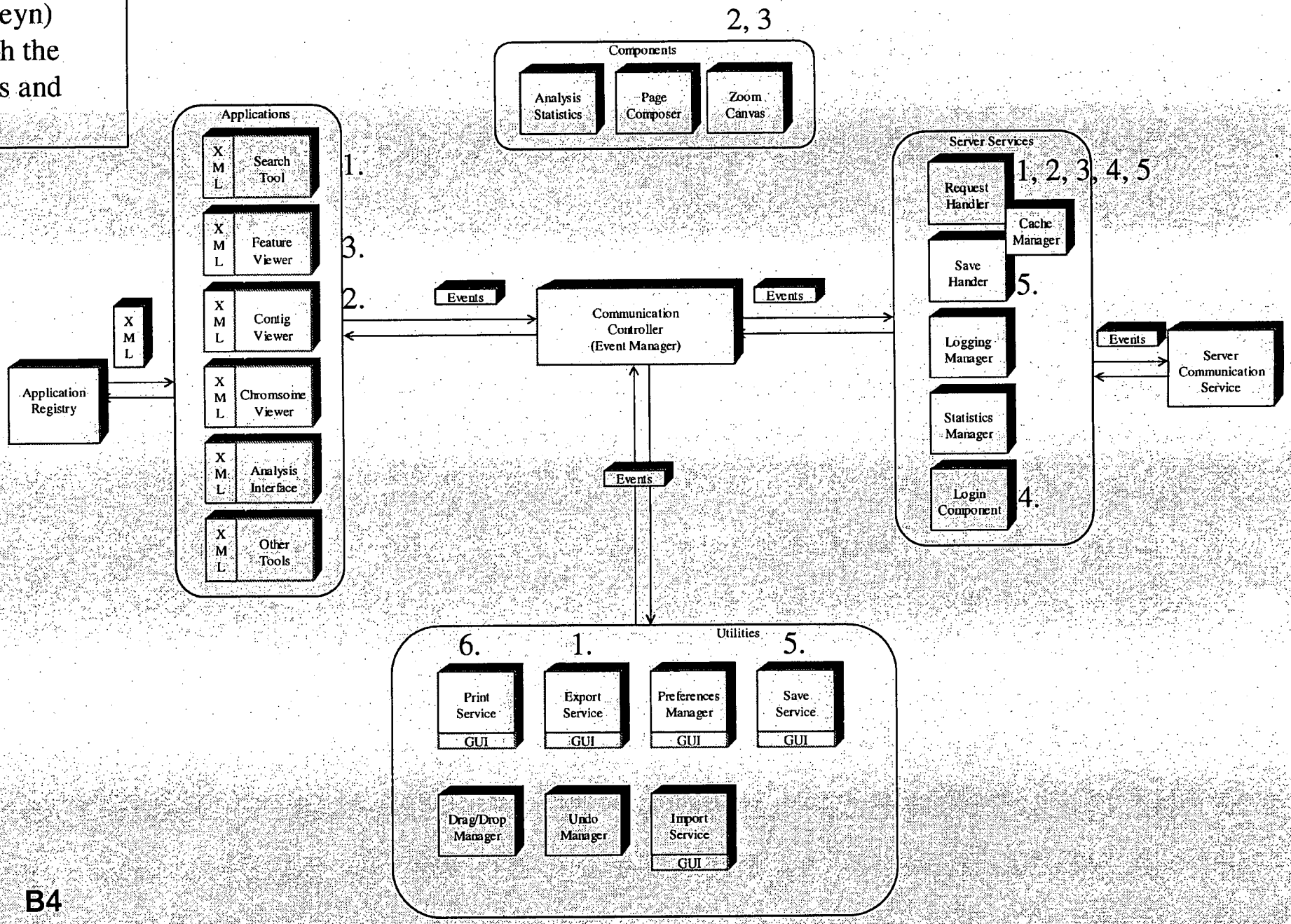


3. Feature Viewer (Chantal Roth)
- shows detailed information about a sequence
- displays features on a sequence such as introns, exons, cds, gene predictions, rnas…
- display is zoomable and scrollable
- shows feature details upon selection



4. Login Panel (E Li)
- enables the users to log in
- create a new user account
-Verifies the user information

ıan Rozensteyn)
ications with the
een contents and
equences)

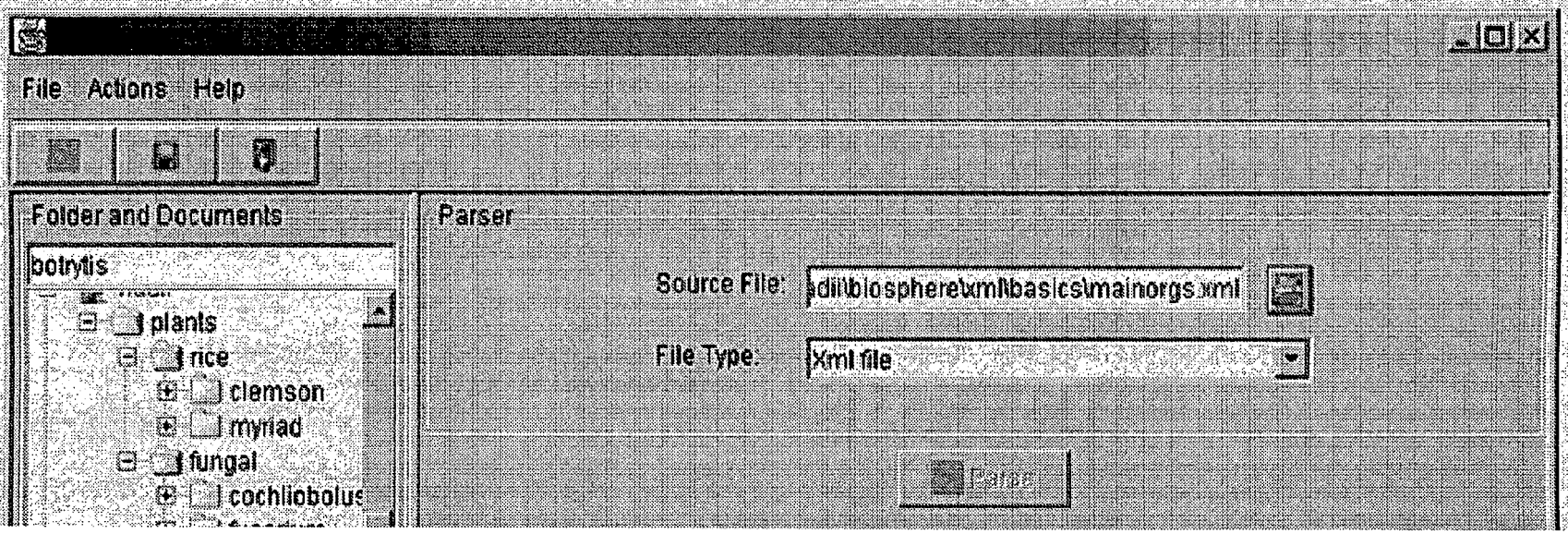


B4

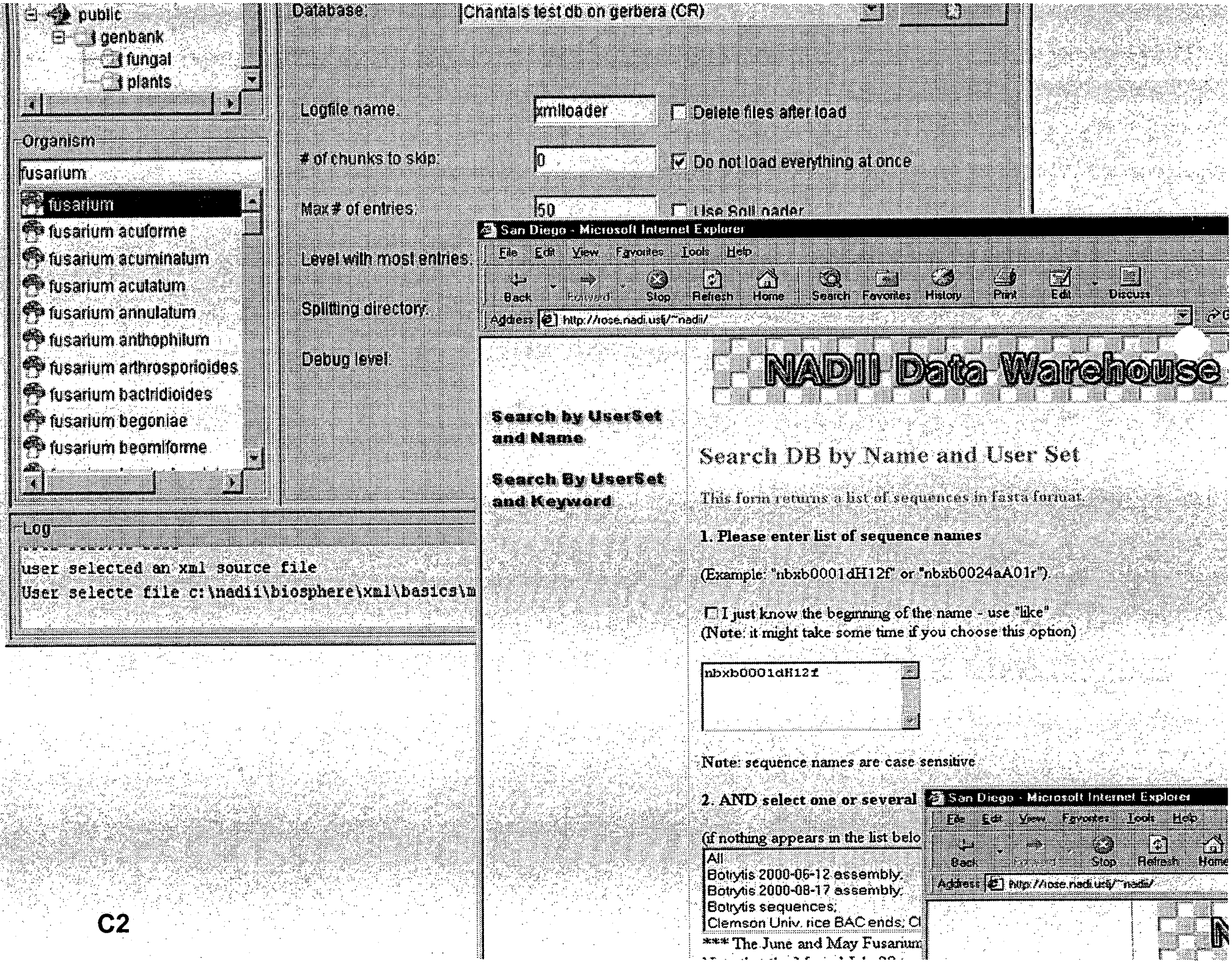
Administration

oman Rozensteyn

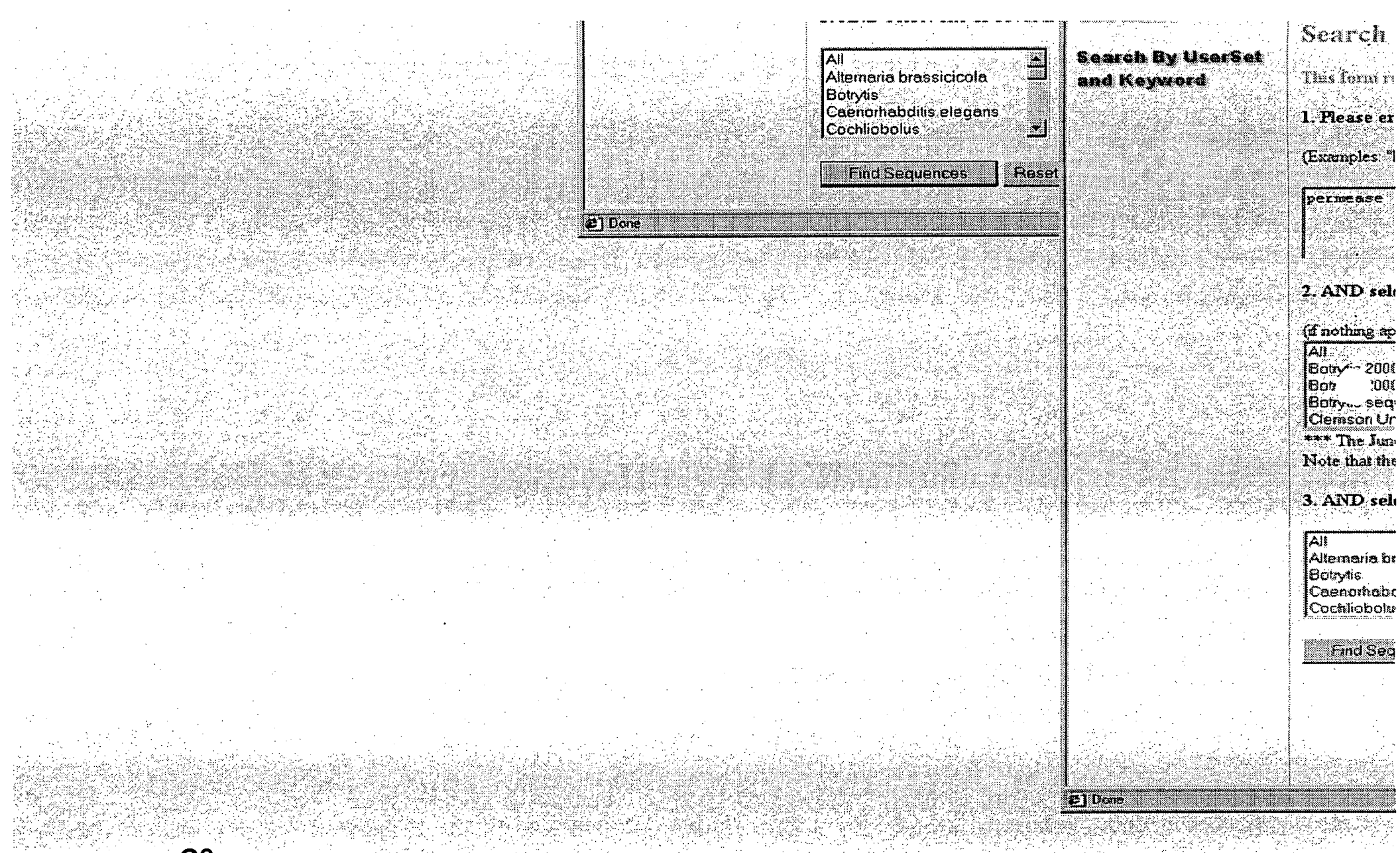
C1



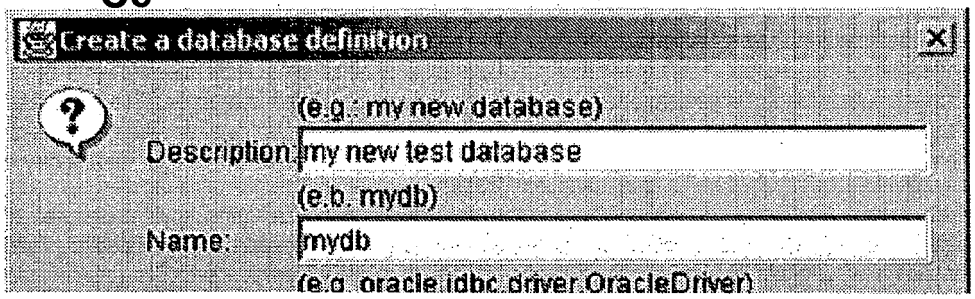
7. Xn
- starts the
- specify p
- select fol
- start xml
- view stat


public
genbank
fungal
plants
Organism
fusarium
fusarium
fusarium acuforme
fusarium acuminatum
fusarium acutatum
fusarium annulatum
fusarium anthophilum
fusarium arthrosporioides
fusarium bactridioides
fusarium begoniae
fusarium beomiforme
Database:
Chantals test db on gerbera (CR)
Logfile name:
xmlloader
Delete files after load
# of chunks to skip:
0
Do not load everything at once
Max # of entries:
50
Level with most entries:
Splitting directory:
Debug level:
Log
user selected an xml source file
User selecte file c:\nadii\biosphere\xml\basics\m
San Diego - Microsoft Internet Explorer
File Edit View Favorites Tools Help
Back Forward Stop Refresh Home Search Favorites History Print Edit Discuss
Address http://rose.nadi.us/~nadii/
NADII Data Warehouse
Search by UserSet and Name
Search By UserSet and Keyword
Search DB by Name and User Set
This form returns a list of sequences in fasta format.
1. Please enter list of sequence names
(Example: "nbxb0001dH12f" or "nbxb0024aA01r").
I just know the beginning of the name - use "like"
(Note: it might take some time if you choose this option)
nbxb0001dH12f
Note: sequence names are case sensitive
2. AND select one or several
(if nothing appears in the list belo
All
Botrytis 2000-06-12 assembly;
Botrytis 2000-08-17 assembly;
Botrytis sequences;
Clemson Univ. rice BAC ends; Cl
*** The June and May Fusarium
San Diego - Microsoft Internet Explorer
File Edit View Favorites Tools Help
Back Stop Refresh Home
Address http://rose.nadi.us/~nadii/

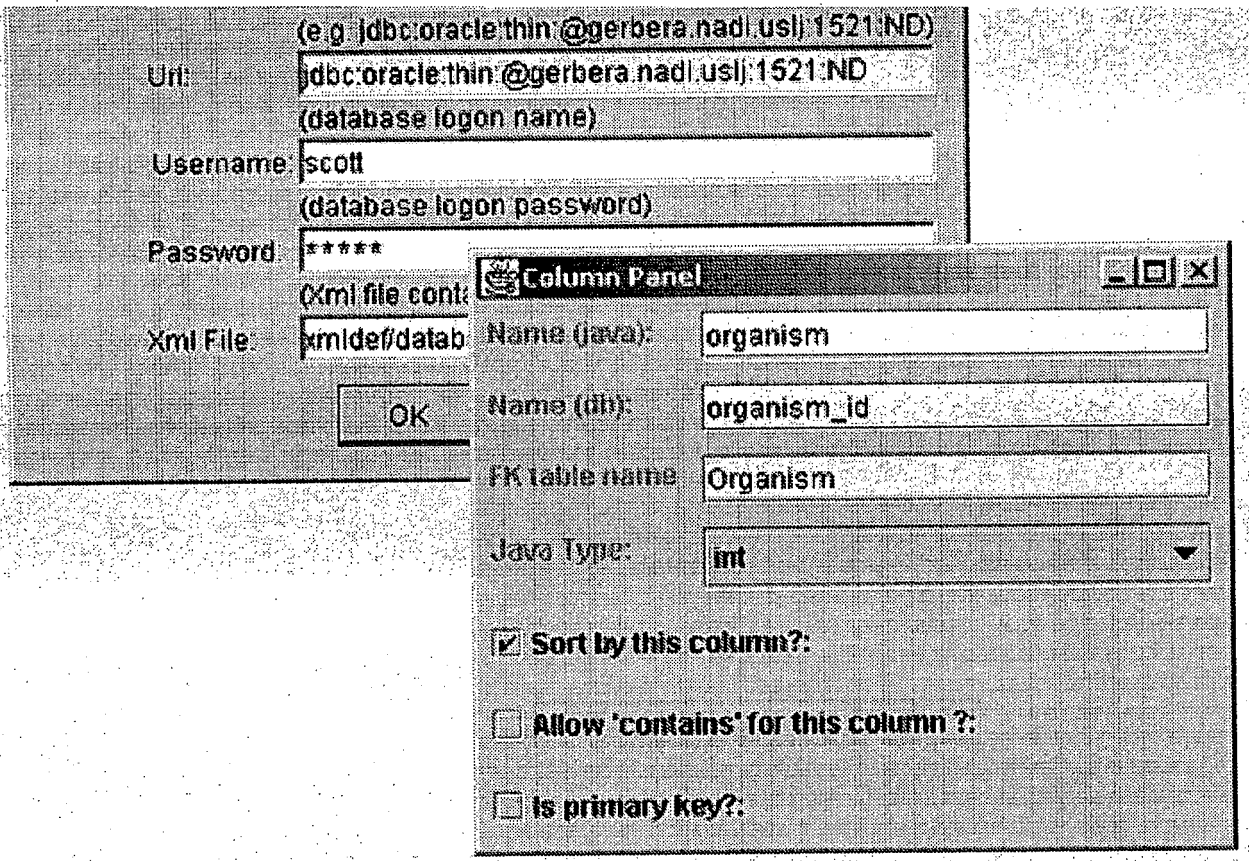
C2



C3



11. Create Database Definitions (Chantal Roth)
- enter parameters for new database
- create database definition data structure that describes this database



12. Data Type Mapping (Chantal R
- map database types to java types
- map database field names to java
- define behavior of column

Tools

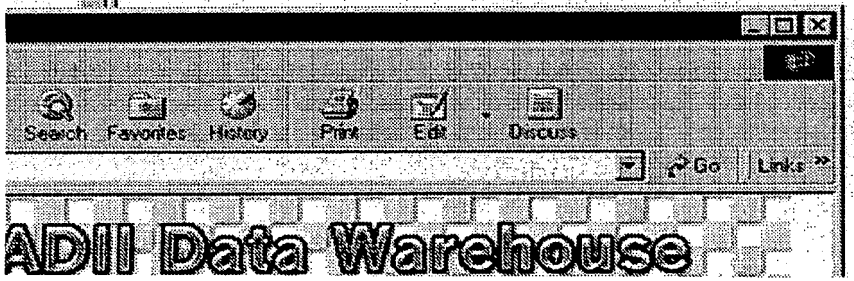
Server

ler Interface (Chantal Roth)
ppropriate parser
ameters for loading
r/organism to save dataset
ader to load data into database
of loading

D1

8. Keyword Search (Chantal Roth)
- search sequences by keyword, organism and folder
- view results in web page
- export sequences to fasta file

D2



9. Name Search (Chantal Roth)
- search sequences by sequence name, organism and folder
- view results in web page
- export sequences to fasta file

B by Keyword and User Set

rns a list of sequences in fasta format.

r list of keywords

ase" or "permease" or "annotransferase").

one or several usersets.

ars in the list below, then the machine is down!)

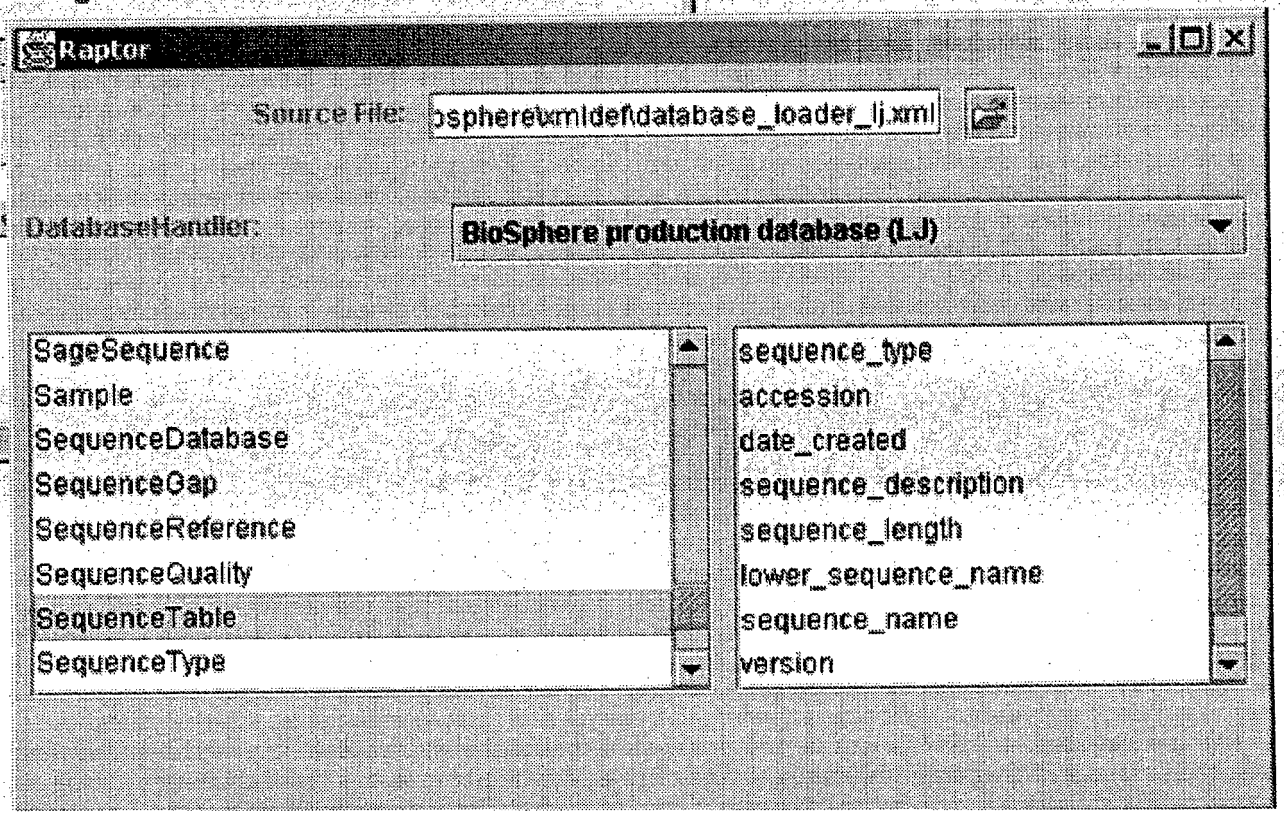
6-12 assembly;
8-17 assembly;
nces;
rice BAC ends; Clemson University rice BAC end sequences
nd May Fusarium assemblies are completely loaded ***
fynad July 28 tape is not completely loaded yet!

one or several organisms.

sicicola
elegans

nces

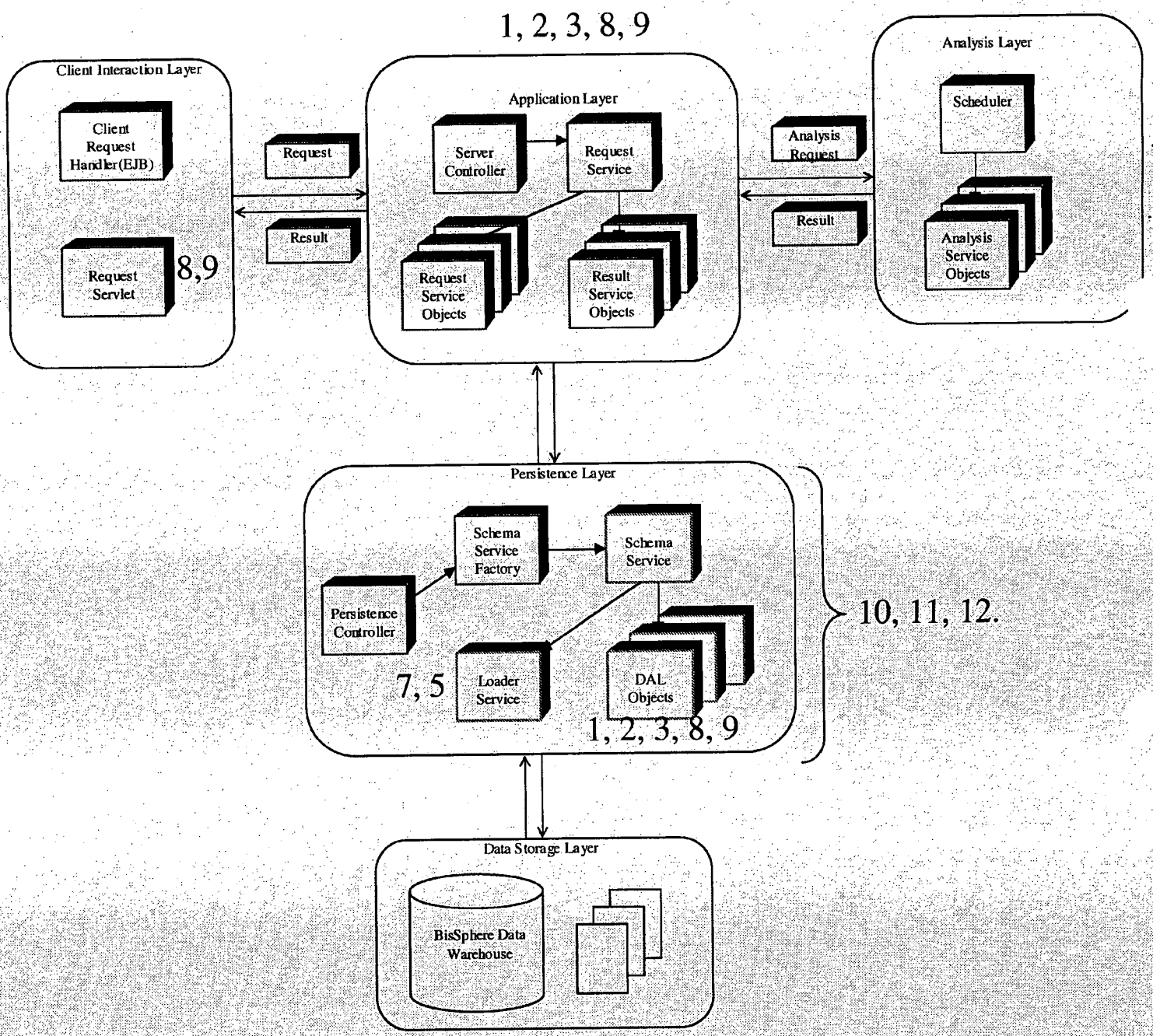
10. O/R Mapping (Chantal Roth)
- create xml definition file from schema
- or create a schema from xml definition file
- create database access classes
- create java bean classes
- create html and xml capable classes



D3

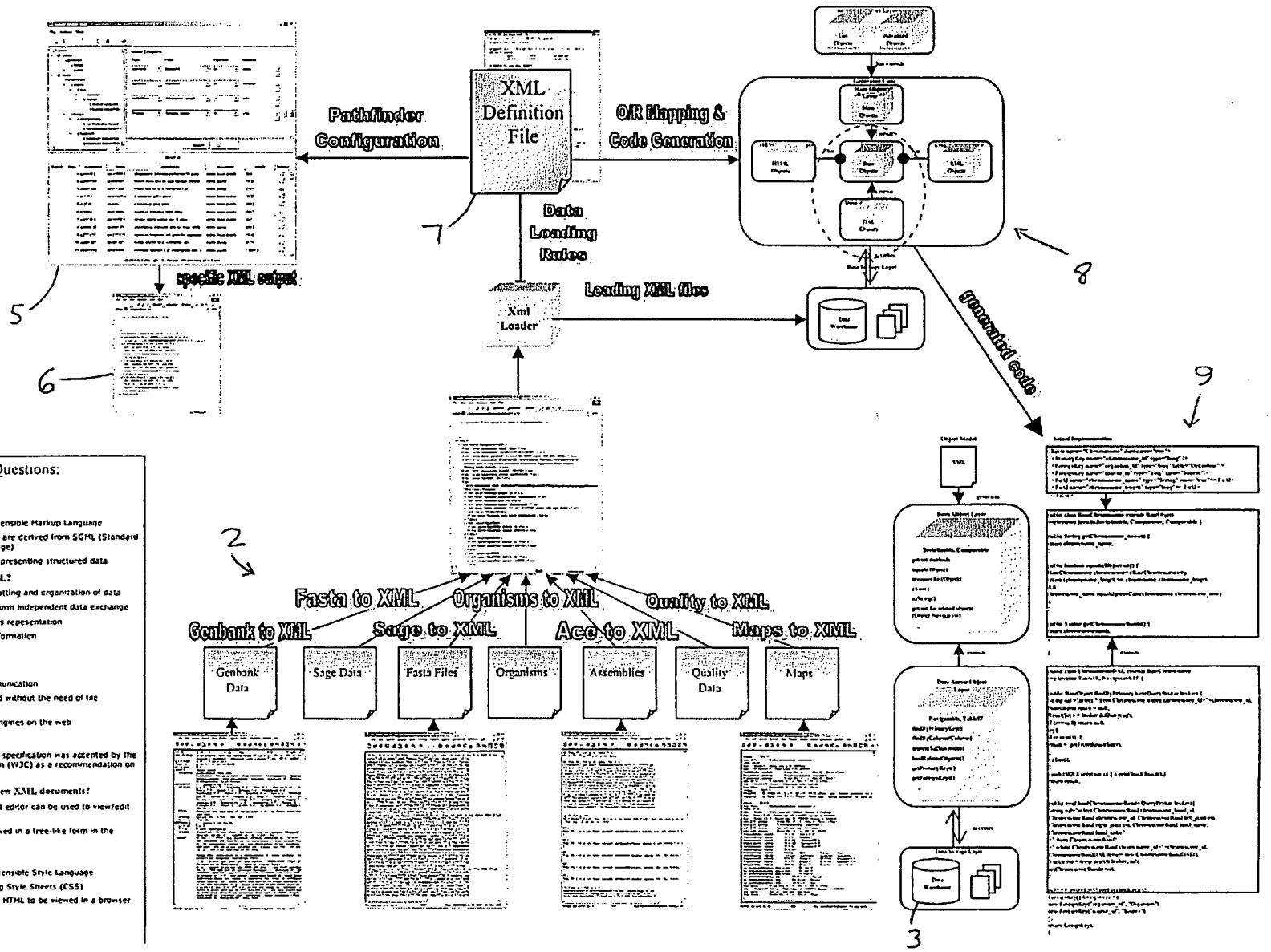
th)

ames


1, 2, 3, 8, 9
Client Interaction Layer
Client Request Handler(EJB)
Request Servlet
8,9
Request
Result
Application Layer
Server Controller
Request Service
Request Service Objects
Result Service Objects
Analysis Request
Result
Analysis Layer
Scheduler
Analysis Service Objects
Persistence Layer
Schema Service Factory
Schema Service
Persistence Controller
7, 5
Loader Service
DAL Objects
1, 2, 3, 8, 9
10, 11, 12.
Data Storage Layer
BisSphere Data Warehouse

D4

Exhibit B



Frequently Asked Questions:

1. What is XML?
- The acronym stands for eXtensible Markup Language
- HTML is also XML, and both are derived from SGML (Standard Generalized Markup Language)
- It is a meta-language for representing structured data

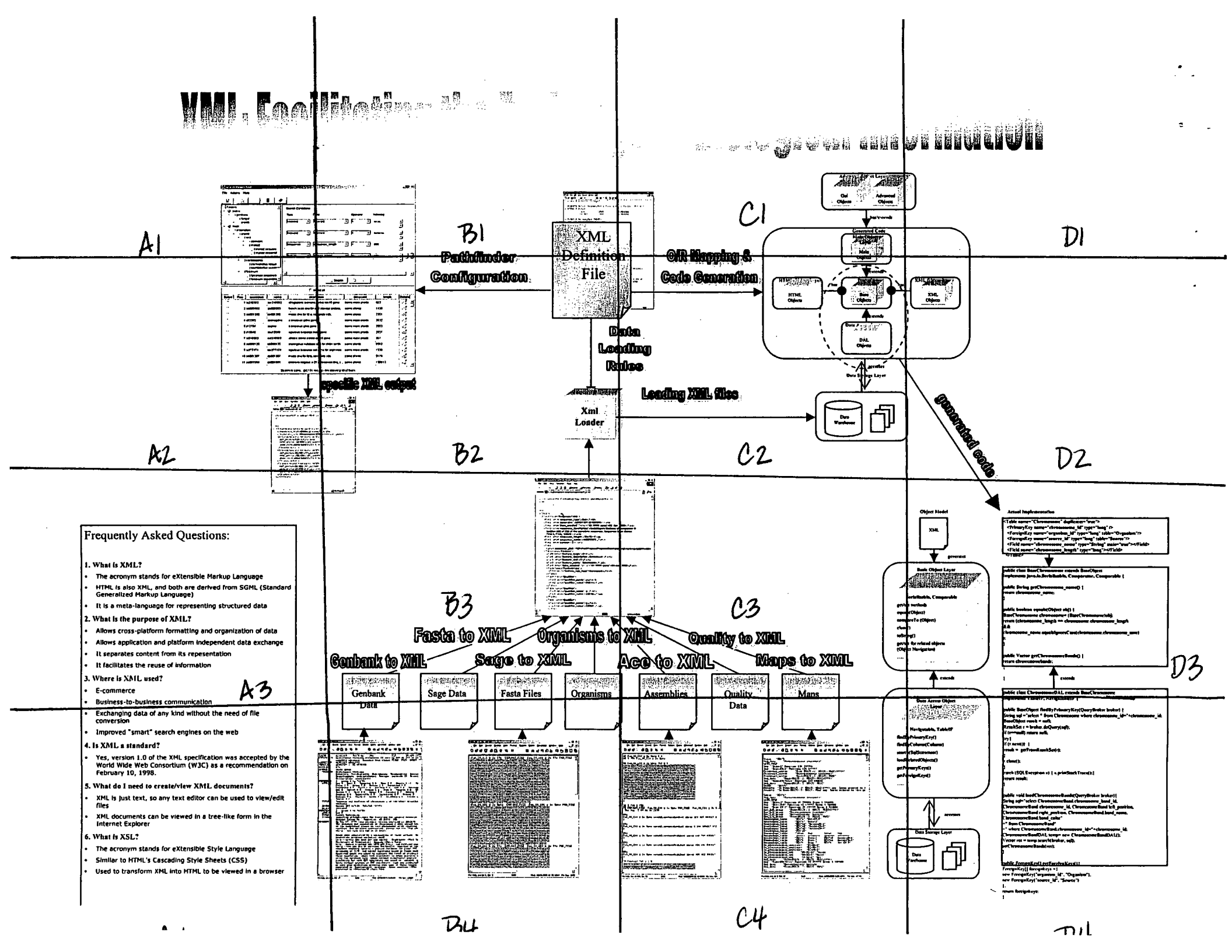
2. What is the purpose of XML?
- Allows cross-platform formatting and organization of data
- Allows application and platform independent data exchange
- It separates content from its representation
- It facilitates the reuse of information

3. Where is XML used?
- E-commerce
- Business-to-business communication
- Exchanging data of any kind without the need of file conversion
- Improved "smart" search engines on the web

4. Is XML a standard?
- Yes, version 1.0 of the XML specification was accepted by the World Wide Web Consortium (W3C) as a recommendation on February 10, 1998.

5. What do I need to create/view XML documents?
- XML is just text, so any text editor can be used to view/edit files
- XML documents can be viewed in a tree-like form in the Internet Explorer

6. What is XSL?
- The acronym stands for eXtensible Style Language
- Similar to HTML's Cascading Style Sheets (CSS)
- Used to transform XML into HTML to be viewed in a browser



Frequently Asked Questions:

1. What is XML?

- The acronym stands for eXtensible Markup Language
- HTML is also XML, and both are derived from SGML (Standard Generalized Markup Language)
- It is a meta-language for representing structured data

2. What is the purpose of XML?

- Allows cross-platform formatting and organization of data
- Allows application and platform independent data exchange
- It separates content from its repesentation
- It facilitates the reuse of information

3. Where is XML used?

- E-commerce
- Business-to-business communication
- Exchanging data of any kind without the need of file conversion
- Improved "smart" search engines on the web

4. Is XML a standard?

- Yes, version 1.0 of the XML specification was accepted by the World Wide Web Consortium (W3C) as a recommendation on February 10, 1998.

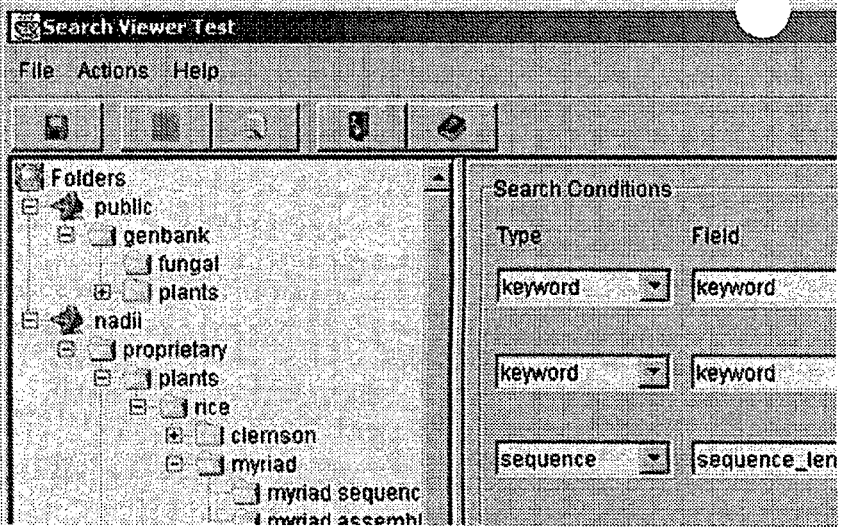
5. What do I need to create/view XML documents?

- XML is just text, so any text editor can be used to view/edit files
- XML documents can be viewed in a tree-like form in the Internet Explorer

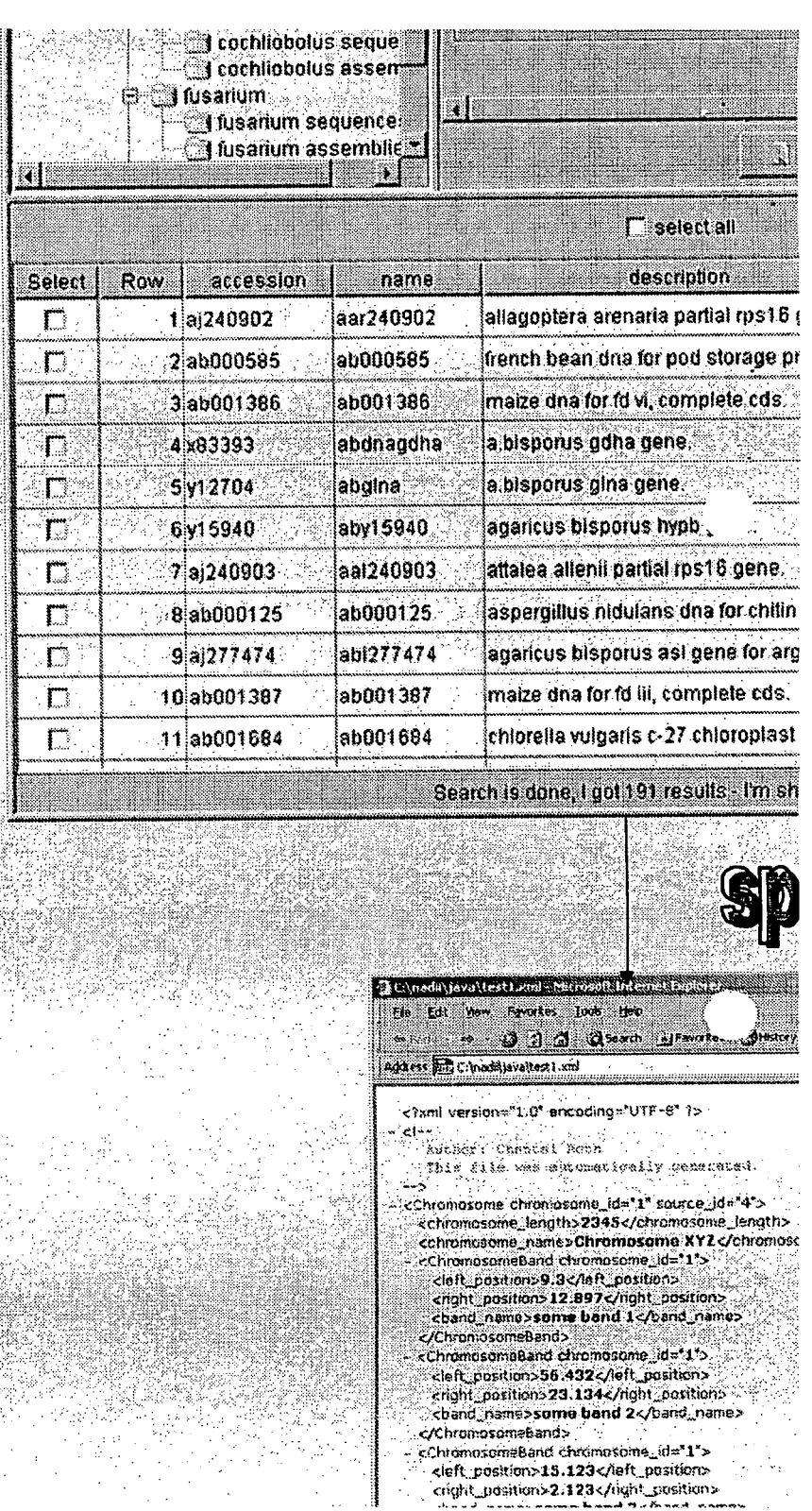
6. What is XSL?

- The acronym stands for eXtensible Style Language
- Similar to HTML's Cascading Style Sheets (CSS)
- Used to transform XML into HTML to be viewed in a browser

XML-faci


Search Viewer Test
File Actions Help
Folders
public
genbank
fungal
plants
nadii
proprietary
plants
rice
clemson
myriad
myriad sequenc
Search Conditions
Type
Field
keyword
keyword
keyword
keyword
sequence
sequence_len

A1


cochliobolus seque
cochliobolus assem
fusarium
fusarium sequence
fusarium assemblie
select all
Select
Row
accession
name
description
1 aj240902 aar240902 allagoptera arenaria partial rps16
2 ab000585 ab000585 french bean dna for pod storage pr
3 ab001386 ab001386 maize dna for fd vi, complete cds.
4 x83393 abdnagdha a.bisporus gdha gene.
5 y12704 abgina a.bisporus gina gene.
6 y15940 aby15940 agaricus bisporus hypb
7 aj240903 aal240903 attalea allenii partial rps16 gene.
8 ab000125 ab000125 aspergillus nidulans dna for chitin
9 aj277474 abi277474 agaricus bisporus asl gene for arg
10 ab001387 ab001387 maize dna for fd iii, complete cds.
11 ab001684 ab001684 chlorella vulgaris c-27 chloroplast
Search is done, I got 191 results - I'm sh
C:\nadi\java\test1.xml - Microsoft Internet Explorer
File Edit View Favorites Tools Help
Address C:\nadi\java\test1.xml
<?xml version="1.0" encoding="UTF-8" ?>
<!--
Author: Chantal Roth
This file was automatically generated.
-->
<Chromosome chromosome_id="1" source_id="4">
<chromosome_length>2345</chromosome_length>
<chromosome_name>Chromosome XYZ</chromosc
<ChromosomeBand chromosome_id="1">
<left_position>9.3</left_position>
<right_position>12.897</right_position>
<band_name>some band 1</band_name>
</ChromosomeBand>
<ChromosomeBand chromosome_id="1">
<left_position>56.432</left_position>
<right_position>23.134</right_position>
<band_name>some band 2</band_name>
</ChromosomeBand>
<ChromosomeBand chromosome_id="1">
<left_position>15.123</left_position>
<right_position>2.123</right_position>

Frequently Asked Questions:

1. What is XML?

- The acronym stands for eXtensible Markup Language
- HTML is also XML, and both are derived from SGML (Standard Generalized Markup Language)
- It is a meta-language for representing structured data

2. What is the purpose of XML?

- Allows cross-platform formatting and organization of data
- Allows application and platform independent data exchange
- It separates content from its repesentation
- It facilitates the reuse of information

3. Where is XML used?

- E-commerce

- Business-to-business communication
- Exchanging data of any kind without the need of file conversion
- Improved "smart" search engines on the web

4. Is XML a standard?

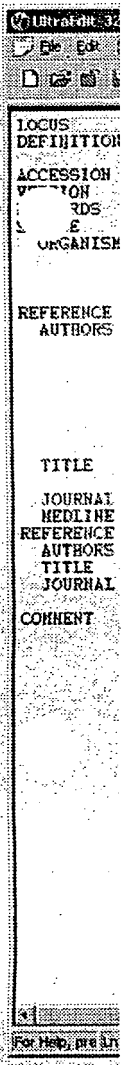
- Yes, version 1.0 of the XML specification was accepted by the World Wide Web Consortium (W3C) as a recommendation on February 10, 1998.

5. What do I need to create/view XML documents?

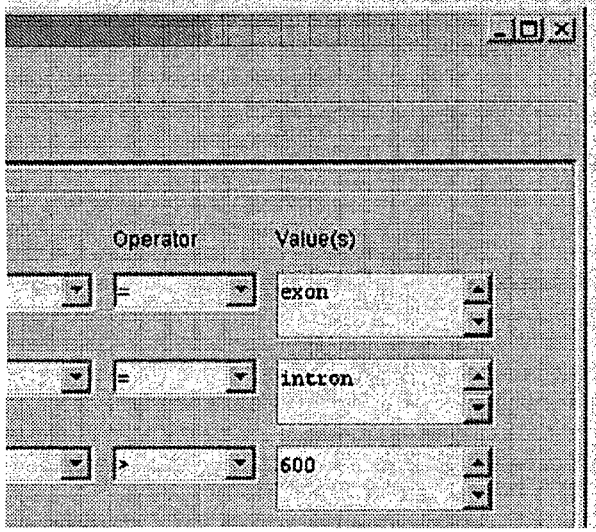
- XML is just text, so any text editor can be used to view/edit files
- XML documents can be viewed in a tree-like form in the Internet Explorer

6. What is XSL?

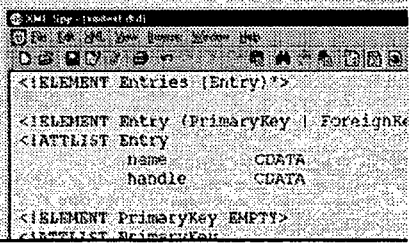
- The acronym stands for eXtensible Style Language
- Similar to HTML's Cascading Style Sheets (CSS)
- Used to transform XML into HTML to be viewed in a browser



tating the Exchang

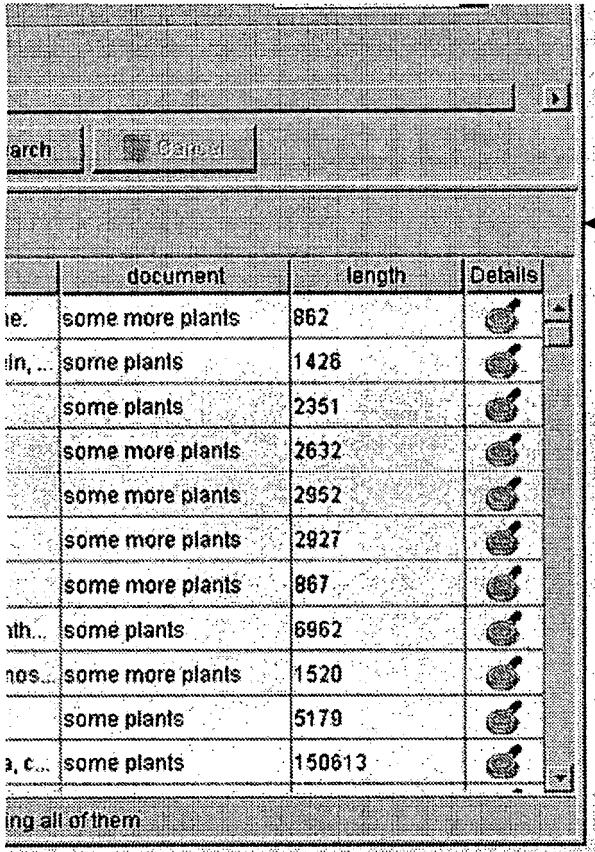


B1



XML

D

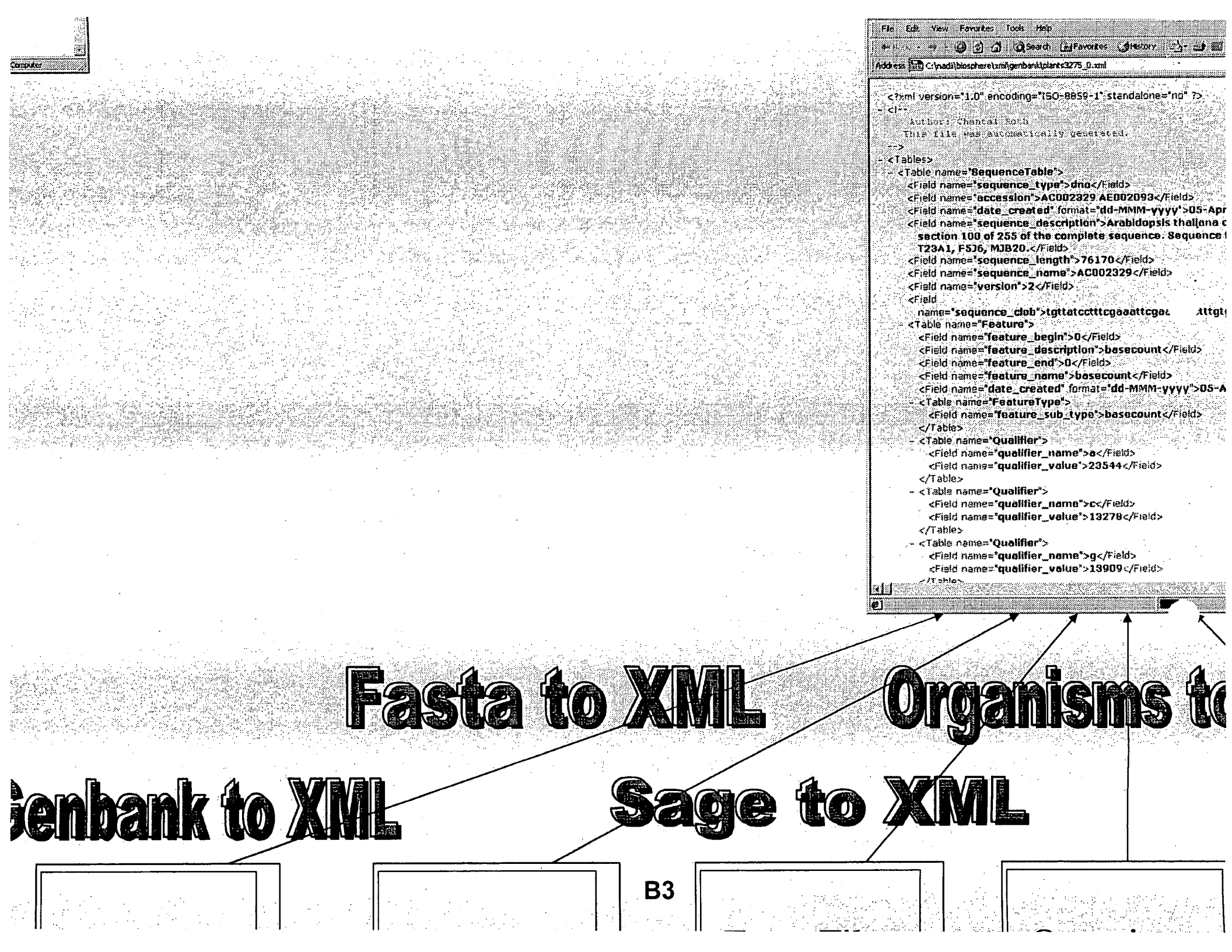


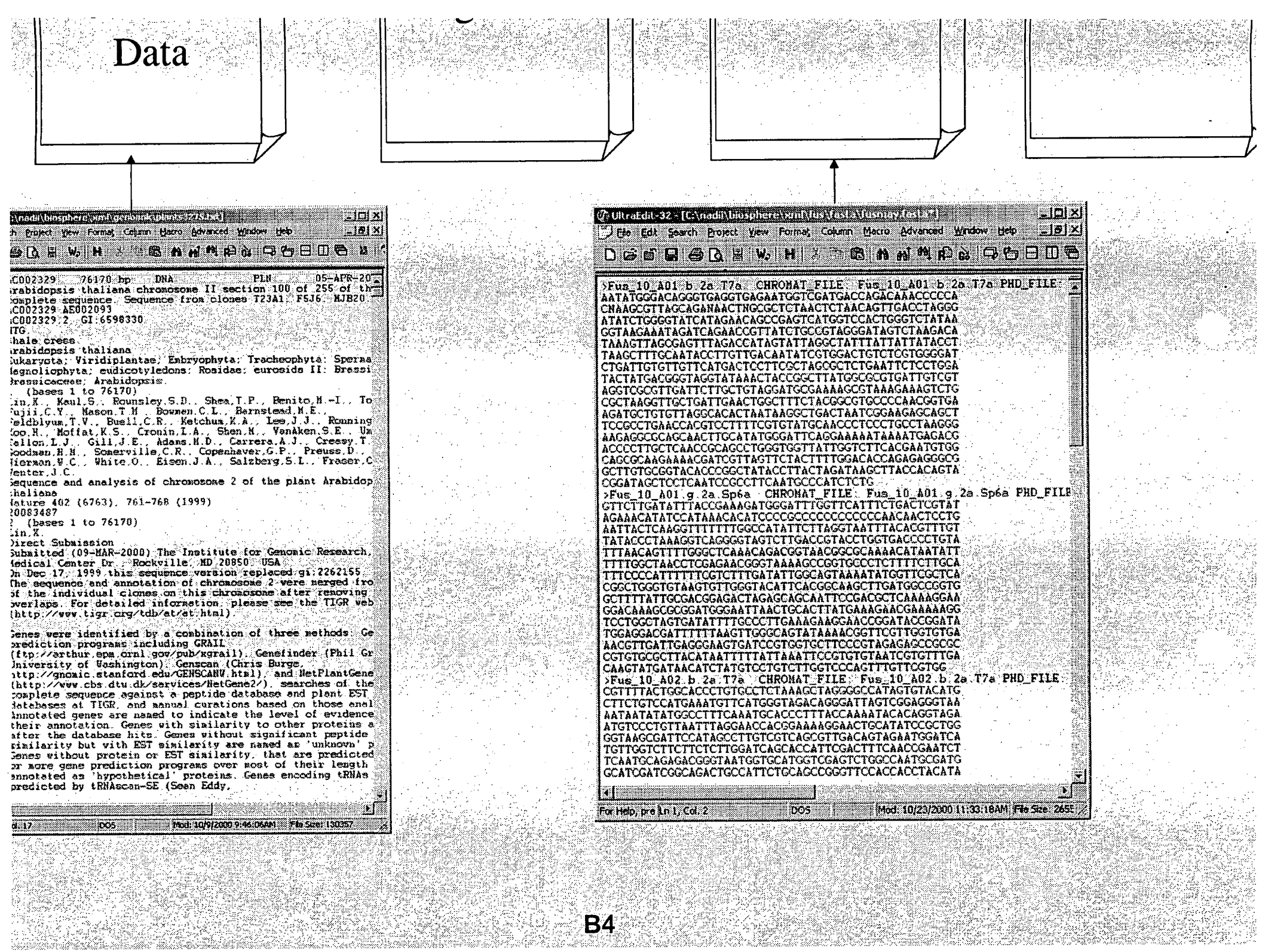
Configuration

File

Xml Loader

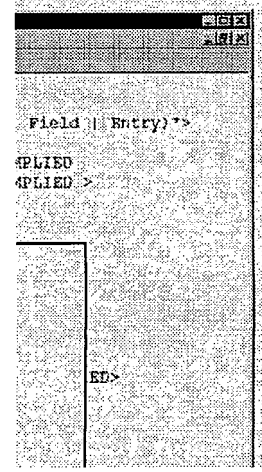
B2

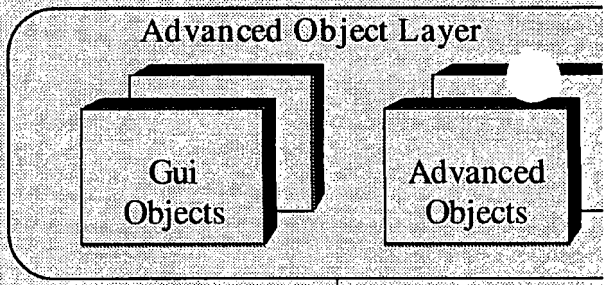

Fasta to XML
Organisms to
enbank to XML
Sage to XML
B3


Data
Project View Format Column Macro Advanced Window Help
iC002329 76170 bp DNA PLN 05-APR-20
rabidopsis thaliana chromosome II section 100 of 255 of th
omplete sequence. Sequence from clones T23A1, F5J6, MJB20
iC002329 AE002093
iC002329.2 GI:6598330
ITG.
:hale cress.
rabidopsis thaliana
ukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sperma
egnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassi
rassicaceae; Arabidopsis.
(bases 1 to 76170)
in,K., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., To
ujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E.,
eldblyum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Rowning
oo,H., Moffat,K.S., Cronin,L.A., Shen,M., VanAken,S.E., Um
ellon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.
oodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D.,
ierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C
enter,J.C.
equence and analysis of chromosome 2 of the plant Arabidop
haliana
ature 402 (6763), 761-768 (1999)
0083487
(bases 1 to 76170)
in,K.
irect Submission
ubmitted (09-MAR-2000) The Institute for Genomic Research,
edical Center Dr., Rockville, MD 20850, USA
n Dec 17, 1999 this sequence version replaced gi:2262155
he sequence and annotation of chromosome 2 were merged fro
f the individual clones on this chromosome after removing
verlaps. For detailed information, please see the TIGR web
(http://www.tigr.org/tdb/at/at.html)
enes were identified by a combination of three methods. Ge
rediction programs including GRAIL
(ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Gr
niversity of Washington), Genscan (Chris Burge,
ttp://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene
(http://www.cbs.dtu.dk/services/NetGene2/), searches of the
omplete sequence against a peptide database and plant EST
atabases at TIGR, and manual curations based on those anal
nnotated genes are named to indicate the level of evidence
their annotation. Genes with similarity to other proteins a
fter the database hits. Genes without significant peptide
imilarity but with EST similarity are named as 'unknown' p
enes without protein or EST similarity, that are predicted
or more gene prediction programs over most of their length
nnotated as 'hypothetical' proteins. Genes encoding tRNAs
redicted by tRNAscan-SE (Sean Eddy,
DOS
Mod: 10/9/2000 9:46:06AM
File Size: 130357
UltraEdit-32
File Edit Search Project View Format Column Macro Advanced Window Help
>Fus_10_A01.b.2a.T7a CHROMAT_FILE: Fus_10_A01.b.2a.T7a PHD_FILE:
AATATGGGACAGGGTGAGGTGAGAATGGTCGATGACCAGACAAACCCCCA
CNAAGCGTTAGCAGANAACTNGCGCTCTAACTCTAACAGTTGACCTAGGG
ATATCTGGGGTATCATAGAACAGCCGAGTCATGGTCCACTGGGTCTATAA
GGTAAGAAATAGATCAGAACCGTTATCTGCCGTAGGGATAGTCTAAGACA
TAAAGTTAGCGAGTTTAGACCATAGTATTAGGCTATTTATTATTATACCT
TAAGCTTTGCAATACCTTGTTGACAATATCGTGGACTGTCTCGTGGGGAT
CTGATTGTGTTGTTCATGACTCCTTCGCTAGCGCTCTGAATTCTCCTGGA
TACTATGACGGGTAGGTATAAACTACCGGCTTATGGCGCGTGATTGTCGT
AGGTCGCGTTGATTCTTGCTGTAGGATGCGAAAAGCGTAAAGAAAGTCTG
CGCTAAGGTTGCTGATTGAACTGGCTTTCTACGGCGTGCCCCAACGGTGA
AGATGCTGTGTTAGGCACACTAATAAGGCTGACTAATCGGAAGAGCAGCT
TCCGCCTGAACCACGTCCTTTTCGTGTATGCAACCCTCCCTGCCTAAGGG
AAGAGGCGCAGCAACTTGCATATGGGATTCAGGAAAAATAAAATGAGACG
ACCCCTTGCTCAACCGCAGCCTGGGTGGTTATTGGTCTTCACGAATGTGG
CAGCGCAAGAAAACGATCGTTAGTTCTACTTTTGGACACCAGAGAGGGCG
GCTTGTGCGGTACACCCGGCTATACCTTACTAGATAAGCTTACCACAGTA
CGGATAGCTCCTCAATCCGCCTTCAATGCCCATCTCTG
>Fus_10_A01.g.2a.Sp6a CHROMAT_FILE: Fus_10_A01.g.2a.Sp6a PHD_FILE:
GTTCTTGATATTTACCGAAAGATGGGATTTGGTTCATTTCTGACTCGTAT
AGAAACATATCCATAAACACATCCCCGCCCCCCCCCCCCCAACAACTCCTG
AATTACTCAAGGTTTTTTTGGCCATATTCTTAGGTAATTTACACGTTTGT
TATACCCTAAAGGTCAGGGGTAGTCTTGACCGTACCTGGTGACCCCTGTA
TTTAACAGTTTTGGGCTCAAACAGACGGTAACGGCGCAAAACATAATATT
TTTTGGCTAACCTCGAGAACGGGTAAAAGCCGGTGCCCTCTTTTCTTGCA
TTTCCCCATTTTTTCGTCTTTGATATTGGCAGTAAAATATGGTTCGCTCA
CGGCTGGGTGTAAGTGTTGGGTACATTCACGGCAAGCTTGATGGCCGGTG
GCTTTTATTGCGACGGAGACTAGAGCAGCAATTCCGACGCTCAAAAGGAA
GGACAAAGCGCGGATGGGAATTAACTGCACTTATGAAAGAACGAAAAAGG
TCCTGGGTAGTGATATTTTGCCCTTGAAAGAAGGAACCGGATACCGGATA
TGGAGGACGATTTTTTAAGTTGGGCAGTATAAAACGGTTCGTTGGTGTGA
AACGTTGATTGAGGGAAGTGATCCGTGGTGCTTCCCGTAGAGAGCCGCGC
CGTGTGCGCTTACATAATTTTTATTAAATTCCGTGTGTAATCGTGTTTGA
CAAGTATGATAACATCTATGTCCTGTCTTGGTCCCAGTTTGTTCGTGG
>Fus_10_A02.b.2a.T7a CHROMAT_FILE: Fus_10_A02.b.2a.T7a PHD_FILE:
CGTTTTACTGGCACCCTGTGCCTCTAAAGCTAGGGGCCATAGTGTACATG
CTTCTGTCCATGAAATGTTCATGGGTAGACAGGGATTAGTCGGAGGGTAA
AATAATATATGGCCTTTCAAATGCACCCTTTACCAAAATACACAGGTAGA
ATGTCCCTGTTAATTTAGGAACCACGGAAAAGGAACTGCATATCCGCTGG
GGTAAGCGATTCCATAGCCTTGTCGTCAGCGTTGACAGTAGAATGGATCA
TGTTGGTCTTCTTCTCTTGGATCAGCACCATTCGACTTTCAACCGAATCT
TCAATGCAGAGACGGGTAATGGTGCATGGTCGAGTCTGGCCAATGCGATG
GCATCGATCGGCAGACTGCCATTCTGCAGCCGGGTTCCACCACCTACATA
For Help, pre Ln 1, Col. 2
DOS
Mod: 10/23/2000 11:33:18AM
File Size: 265

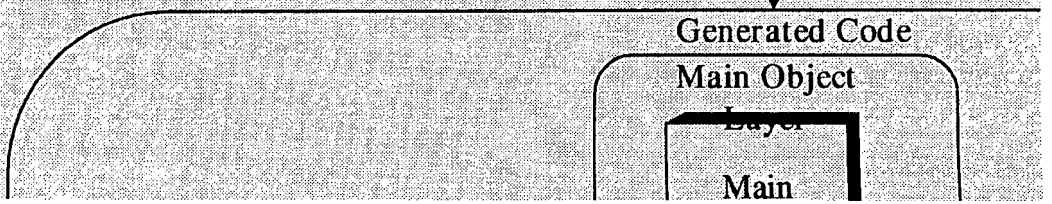
B4

...e of Biological Inf...

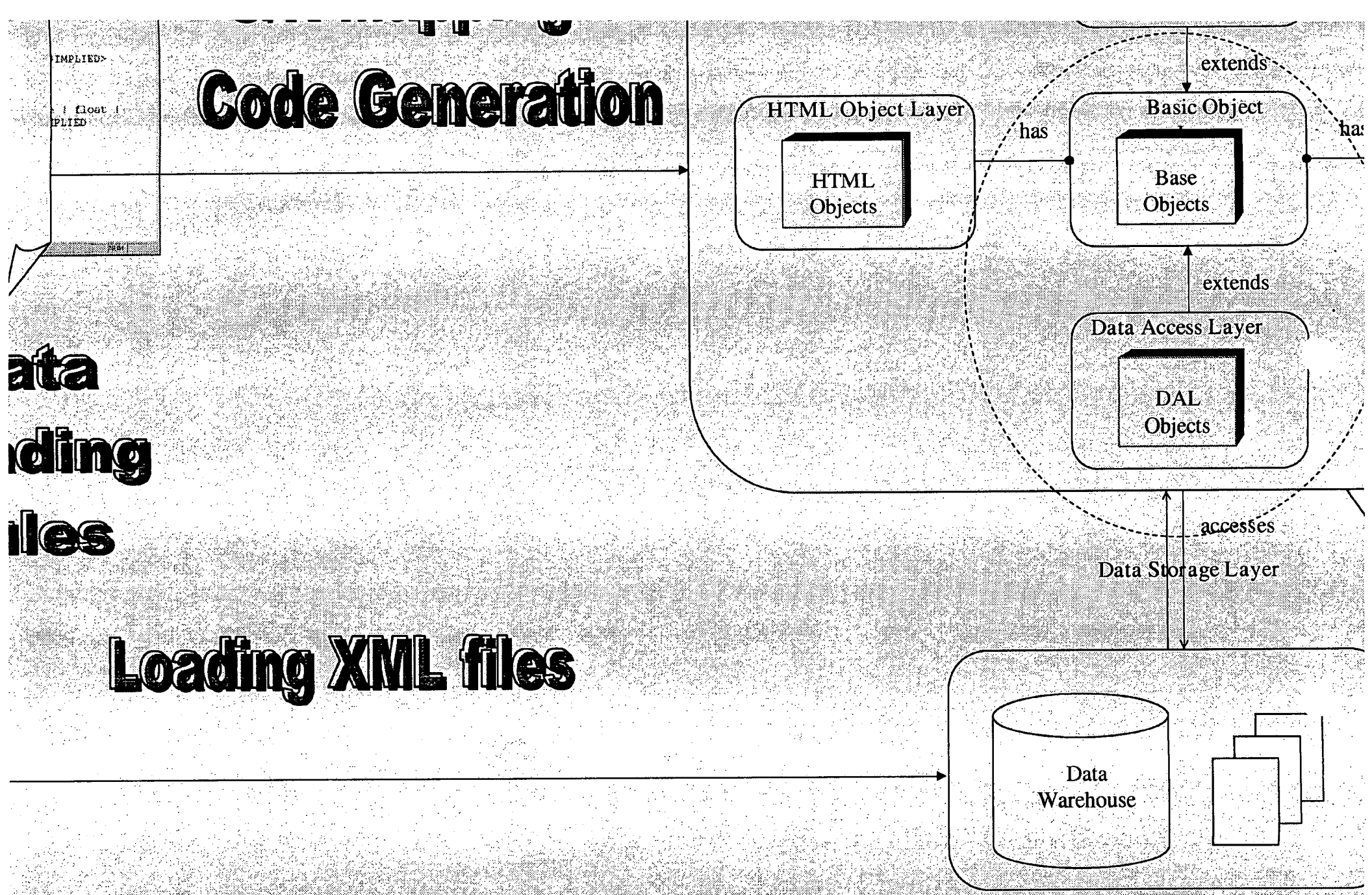




has/extends

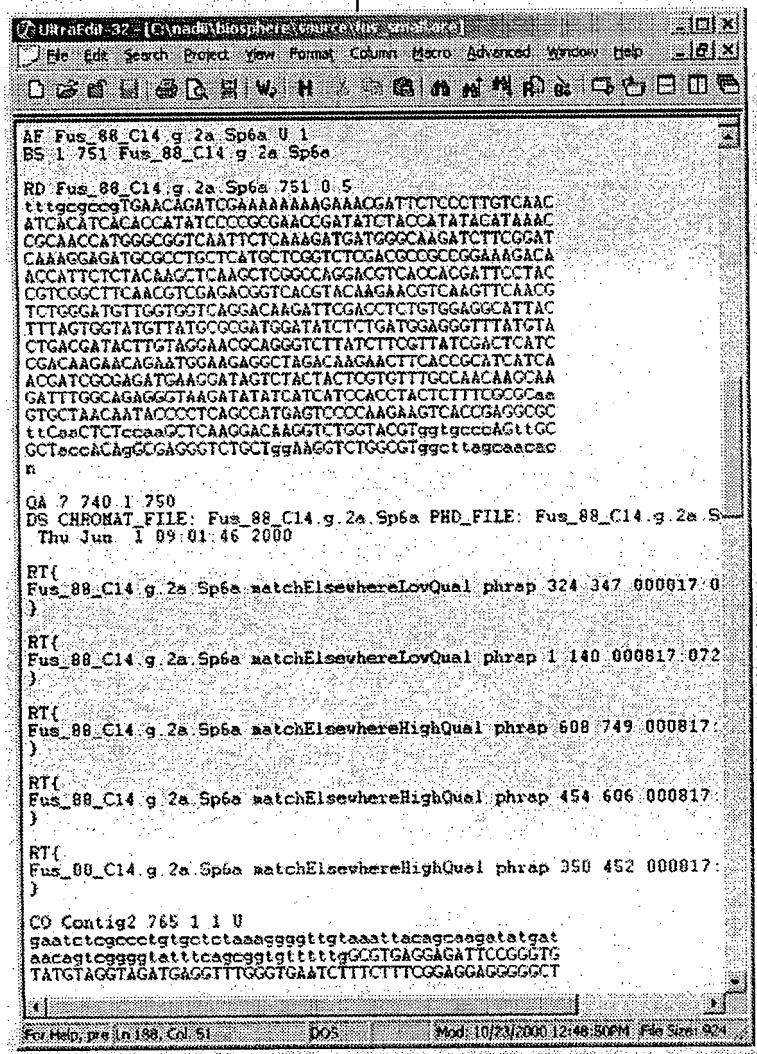


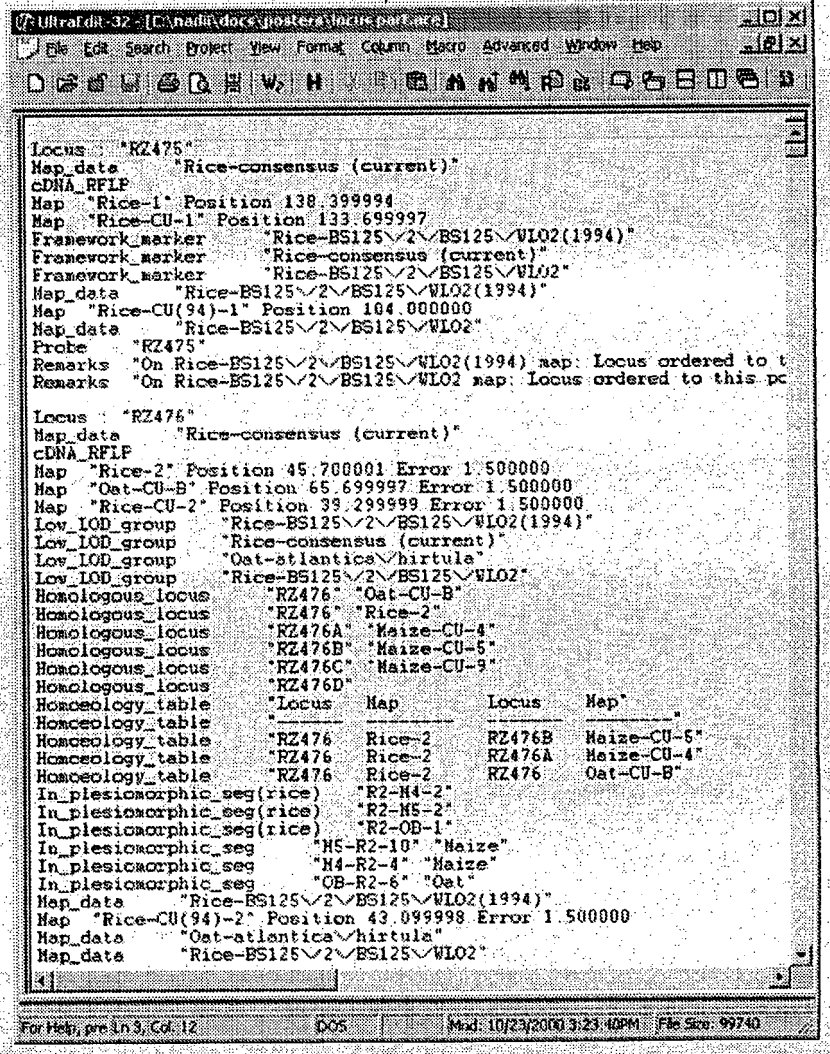
C1


IMPLIED>
float
IPLIED
Code Generation
ata
ding
iles
HTML Object Layer
HTML
Objects
has
Basic Object
Base
Objects
has
extends
extends
Data Access Layer
DAL
Objects
accesses
Data Storage Layer
Loading XML files
Data
Warehouse

XML
Quality to XML
Ace to XML
Maps to XML
C3

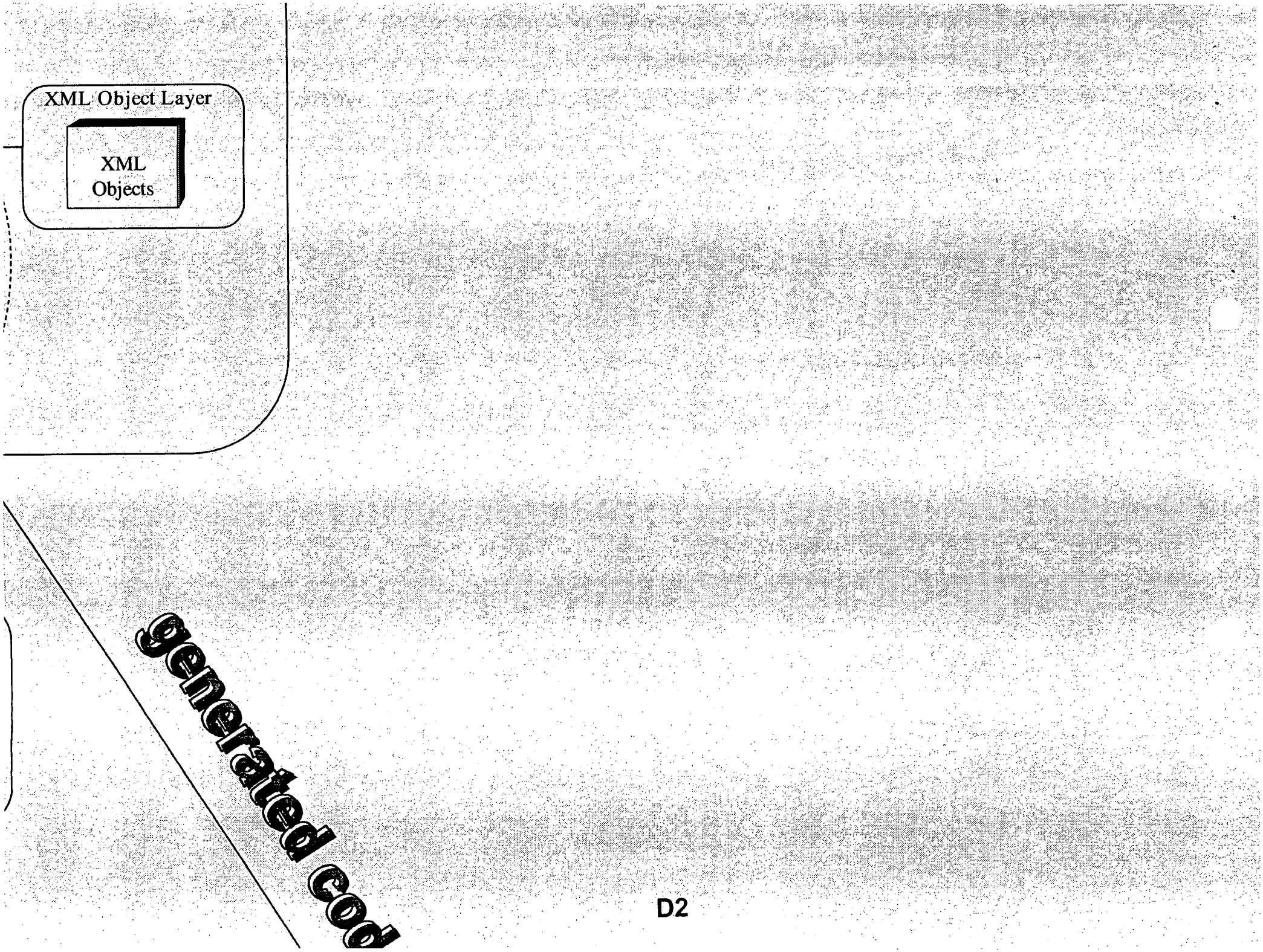
Data

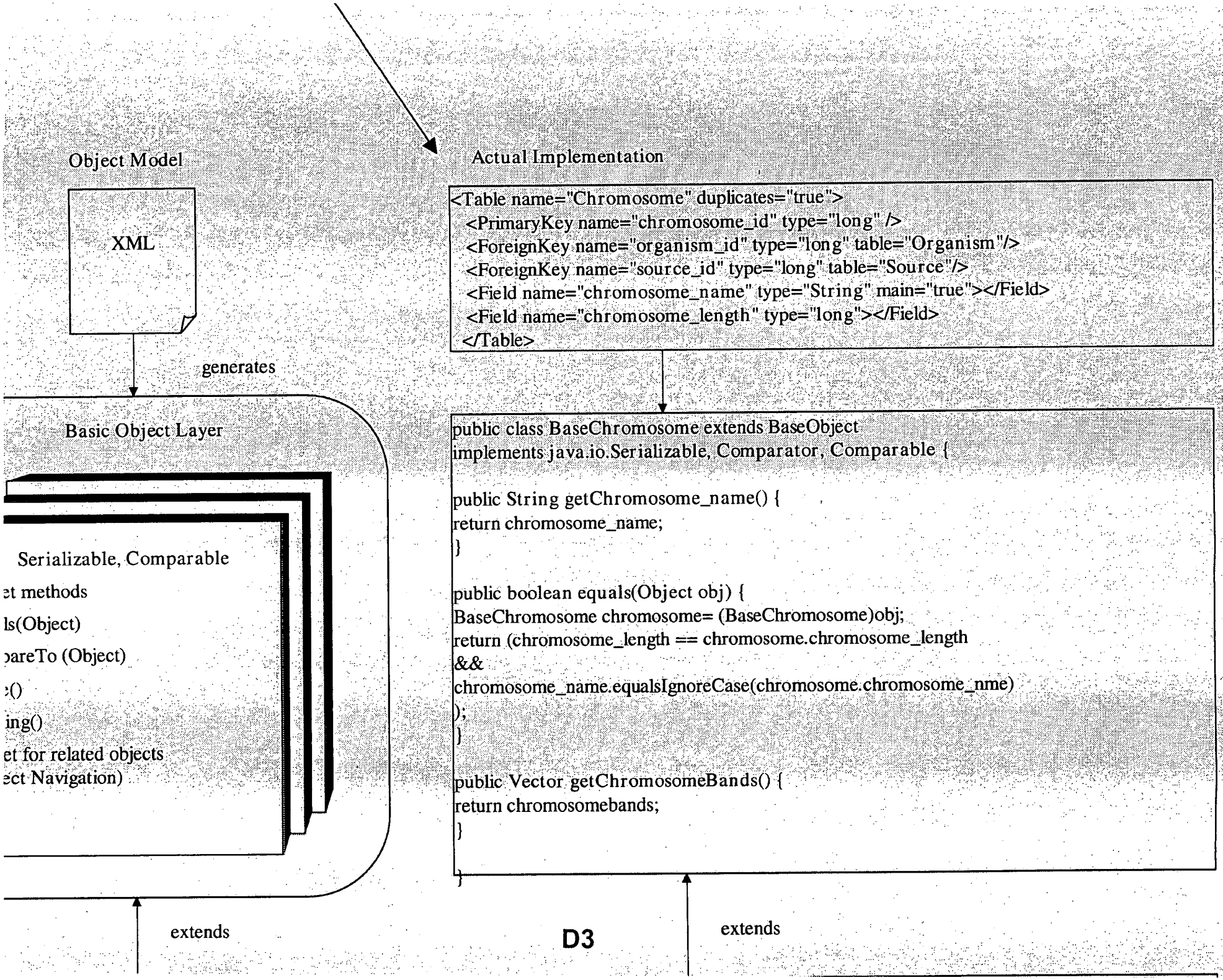

AF Fus_88_C14_g_2a_Sp6a U 1
BS 1 751 Fus_88_C14_g_2a_Sp6a
RD Fus_88_C14_g_2a_Sp6a 751 0 5
QA 7 740 1 750
DS CHROMAT_FILE: Fus_88_C14_g_2a_Sp6a PHD_FILE: Fus_88_C14_g_2a_S
Thu Jun 1 09:01:46 2000
RT{
Fus_88_C14_g_2a_Sp6a matchElsewhereLowQual phrap 324 347 000017 0
}
RT{
Fus_88_C14_g_2a_Sp6a matchElsewhereLowQual phrap 1 140 000817 072
}
RT{
Fus_88_C14_g_2a_Sp6a matchElsewhereHighQual phrap 608 749 000817
}
RT{
Fus_88_C14_g_2a_Sp6a matchElsewhereHighQual phrap 454 606 000817
}
RT{
Fus_88_C14_g_2a_Sp6a matchElsewhereHighQual phrap 350 452 000817
}
CO Contig2 765 1 1 U


Locus : "RZ475"
Map_data "Rice-consensus (current)"
cDNA_RFLP
Map "Rice-1" Position 138.399994
Map "Rice-CU-1" Position 133.699997
Framework_marker "Rice-BS125\/2\/BS125\/WLO2(1994)"
Framework_marker "Rice-consensus (current)"
Framework_marker "Rice-BS125\/2\/BS125\/WLO2"
Map_data "Rice-BS125\/2\/BS125\/WLO2(1994)"
Map "Rice-CU(94)-1" Position 104.000000
Map_data "Rice-BS125\/2\/BS125\/WLO2"
Probe "RZ475"
Remarks "On Rice-BS125\/2\/BS125\/WLO2(1994) map: Locus ordered to t
Remarks "On Rice-BS125\/2\/BS125\/WLO2 map: Locus ordered to this pc
Locus : "RZ476"
Map_data "Rice-consensus (current)"
cDNA_RFLP
Map "Rice-2" Position 45.700001 Error 1.500000
Map "Oat-CU-B" Position 65.699997 Error 1.500000
Map "Rice-CU-2" Position 39.299999 Error 1.500000
Low_LOD_group "Rice-BS125\/2\/BS125\/WLO2(1994)"
Low_LOD_group "Rice-consensus (current)"
Low_LOD_group "Oat-atlantica\/hirtula"
Low_LOD_group "Rice-BS125\/2\/BS125\/WLO2"
Homologous_locus "RZ476" "Oat-CU-B"
Homologous_locus "RZ476" "Rice-2"
Homologous_locus "RZ476A" "Maize-CU-4"
Homologous_locus "RZ476B" "Maize-CU-5"
Homologous_locus "RZ476C" "Maize-CU-9"
Homologous_locus "RZ476D"
Homceology_table "Locus" "Map" "Locus" "Map"
Homceology_table "------" "-------" "-------" "--------"
Homceology_table "RZ476" "Rice-2" "RZ476B" "Maize-CU-5"
Homceology_table "RZ476" "Rice-2" "RZ476A" "Maize-CU-4"
Homceology_table "RZ476" "Rice-2" "RZ476" "Oat-CU-B"
In_plesiomorphic_seg(rice) "R2-M4-2"
In_plesiomorphic_seg(rice) "R2-M5-2"
In_plesiomorphic_seg(rice) "R2-OB-1"
In_plesiomorphic_seg "M5-R2-10" "Maize"
In_plesiomorphic_seg "M4-R2-4" "Maize"
In_plesiomorphic_seg "OB-R2-6" "Oat"
Map_data "Rice-BS125\/2\/BS125\/WLO2(1994)"
Map "Rice-CU(94)-2" Position 43.099998 Error 1.500000
Map_data "Oat-atlantica\/hirtula"
Map_data "Rice-BS125\/2\/BS125\/WLO2"

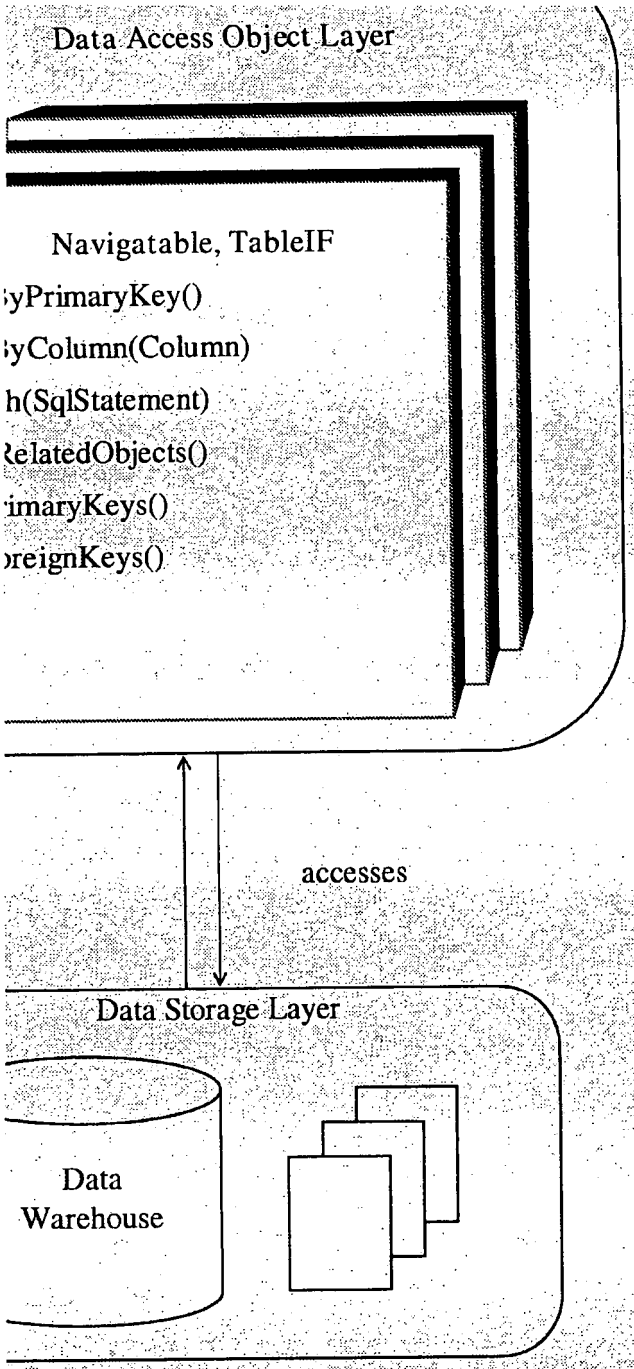
C4

ormation


XML Object Layer
XML Objects
generated cod
D2


Object Model
XML
generates
Actual Implementation
<Table name="Chromosome" duplicates="true">
<PrimaryKey name="chromosome_id" type="long" />
<ForeignKey name="organism_id" type="long" table="Organism"/>
<ForeignKey name="source_id" type="long" table="Source"/>
<Field name="chromosome_name" type="String" main="true"></Field>
<Field name="chromosome_length" type="long"></Field>
</Table>
Basic Object Layer
Serializable, Comparable
et methods
ls(Object)
pareTo (Object)
:()
ing()
et for related objects
ect Navigation)
public class BaseChromosome extends BaseObject
implements java.io.Serializable, Comparator, Comparable {
public String getChromosome_name() {
return chromosome_name;
}
public boolean equals(Object obj) {
BaseChromosome chromosome= (BaseChromosome)obj;
return (chromosome_length == chromosome.chromosome_length
&&
chromosome_name.equalsIgnoreCase(chromosome.chromosome_nme)
);
}
public Vector getChromosomeBands() {
return chromosomebands;
}
}
extends
extends

D3




```
implements TableIF, Navigatable {

public BaseObject findByPrimaryKey(QueryBroker broker) {
String sql ="select * from Chromosome where chromosome_id="+chromosome_id;
BaseObject result = null;
ResultSet r = broker.doQuery(sql);
if (r==null) return null;
try{
if (r.next()) {
result =  getFromResultSet(r);
}
r.close();
}
catch (SQLException x) { x.printStackTrace();}
return result;
}

public void loadChromosomeBands(QueryBroker broker){
String sql="select ChromosomeBand.chromosome_band_id,
ChromosomeBand.chromosome_id, ChromosomeBand.left_position,
ChromosomeBand.right_position, ChromosomeBand.band_name,
ChromosomeBand.band_color"
+" from ChromosomeBand"
+" where ChromosomeBand.chromosome_id="+chromosome_id;
ChromosomeBandDAL temp= new ChromosomeBandDAL();
Vector res = temp.search(broker, sql);
setChromosomeBands(res);
}

public ForeignKey[] getForeignKeys(){
ForeignKey[] foreignkeys ={
new ForeignKey("organism_id", "Organism"),
new ForeignKey("source_id", "Source")
};
return foreignkeys;
}
```

This Page is Inserted by IFW Indexing and Scanning Operations and is not part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☑ FADED TEXT OR DRAWING
- ☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☐ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.
As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.